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(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

(57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the

oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostatic cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ⁹⁰Y, ¹²³I, ¹²⁵I, ¹³¹I, ¹⁸⁶Re, ¹⁸⁸Re, ²¹¹At, and ²¹²Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (*i.e.*, untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size

being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library(prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ

ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTON

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant

homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun
Dillon, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

(iv) CORRESPONDENCE ADDRESS:

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(F) ZIP: 98104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 23-FEB-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.428C3

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTTCACAG TATAACAGCT CTTTATTTCT GTGAGTTCTA CTAGGAAATC

ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATAACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGTC	CAGTCCCCTCT	CCTTAACCTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCCTCC	180
CTCCCTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCCTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGGCCACCGCG	GTGGAGCTCC	AGCTTTGTG	CCCTTTAGTG	AGGGTTAATT	420
GCCCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	480
ATTCCACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTTGCGCTCA	CTGNCCGCTT	TCCAGTCNGG	AAAACGTGCG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAAA	GCGGTTTGC	TTT'CGGGGGC	660
TCTTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCTNT	CGGCTGCGGG	GAACGGTATC	720
ACTCCTAAA	GGNGGTATTA	CGGTTATCCN	NAAATCNGGG	GATACCCNGG	AAAAAAANTTT	780
ACAAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAA			814

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATACGACTT	ACAGGACAGC	AGATGGGAA	60
TTCATGGCTG	TTGGAGCAAT	AGAACCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTTGGA	120
CTAAAGTCTG	ATGAACTTCC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGAG	ATGTATTTC	AAAGAAGACG	AAGGCAGAGT	GGTGTCAAAT	CTTGACGGC	240
ACAGATGCC	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTCATCA	TGATCACAAC	300
AAGGAACGGG	GCTCGTTAT	CACCAGTGAG	GAGCAGGACG	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTTAA	ACACCCAGC	CATCCCTTCT	TTCAAAAGGG	ATCCACTAGT	TCTAGAAGCG	420
GCCGCCACCG	CGGTGGAGCT	CCAGCTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTCCCTGT	GTGAAATTGT	TATCCGCTCA	CAATTCCCCC	540
AACATACGAG	CCGGAACATA	AAGTGTAAAG	CCTGGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTTGCGCTCA	CTGCCGCTT	TCCAGTCGGG	AAAACGTGCG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCC	CGGGAAAAGG	CGGTTGCNTT	TTGGGCTCT	TCCGCTTCC	720
TCGCTCATTG	ATCCCTNGNC	CCGGTCTTCG	GCTGCGGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNTNCCGG	TTATCCCCAA	ACNGGGATA	CCNGA			816

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG	AAGGGATGGC	TGGGGTGT	AACAGCAGAG	GTGCAGGGCG	GGGGCTCACC	50
TCCTGCTCCT	CACTGGTGAT	AAACGAGCCC	CGTTCCCTGT	TGTGATCATG	ATGAACAAACC	120

TCCTCAAAAG	TCAGAACCGG	AGTCACACAG	GCATCTGTGC	CGTCAAAGAT	TTGACACCAC	180
TCTGCCCTCG	TCTTCCTTGC	AAATAACATCT	GCAAACATTCT	TCTTCATTT	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTTCATCA	GACTTTAGTC	CANNTCTTT	GATCAGCAGC	300
TCGTAGAACT	GGGGTTCTAT	TGCTCCAACA	GCCATGAATT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTG	CTCGAGGGGG	GGCCCGGTAC	420
CCAATTGCC	CTATANTGAG	TCGTATTACG	CGCGCTCACT	GGCCGTGTT	TTACAACGTC	480
GTGACTGGGA	AAACCCCTGGG	CGTTACCAAC	TTAATCGCCT	TGCAGCACAT	CCCCCTTTCG	540
CCAGCTGGGC	CTAATANCAGA	AAAGGCCGC	ACCGATGCC	CTTCCAACAG	TTGCGCACCT	600
GAATGGGNA	ATGGGACCCC	CCTGTTACCG	CGCATTNAAC	CCCCGCNNGG	TTTNGTTGTT	660
ACCCCCACNT	NNACCGCTTA	CACTTTGCCA	GCGCCTTANC	GCCCGCTCCC	TTICNCCTTT	720
CTTCCCTTCC	TTTCNCNNCN	CTTTCCCCG	GGGTTTCCCC	CNTCAAACCC	CNA	773

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGAGT	CCTACTGACC	TGTGCTTCT	GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTC	GTCTCTCCT	120
TCGGAACACT	GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAAG	180
ACGTGGGTGA	CCATGTTGTT	TGTGGGGTGC	AGAGATGGGA	GGGGTGGGGC	CCACCCCTGGA	240
AGAGTGGACA	GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGCATG	AGGCACACAC	ACAGCAAGGA	TGACNTGTA	AACATAGCCC	ACGCTGTCCT	360
GNGGGCACTG	GGAAGCCTAN	ATNAGGCCGT	GAGCANAAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGANCTCC	ANCTTTTGTT	CCCTTTAGTG	AGGGTTAATT	480
GCGCGCTTGG	CNTAATCATG	GTCATANCTN	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	540
ATTCCACACA	ACATACGANC	CGGAAACATA	AANTGTAAAC	CTGGGGTGCC	TAATGANTGA	600
CTAACTCACA	TTAATTGCGT	TGCGCTACT	GCCCCCTTTC	CAATCNGGAA	ACCTGTCTTG	660
CCNCTTGCAT	TNATGAATCN	GCCAACCCCC	GGGGAAAAGC	TTTGCGTTT	TGGCGCTCT	720
TCCGCTTCCCT	CNCTCANTTA	NTCCCTNCNC	TCGGTCATTC	CGGCTGCNGC	AAACCGGTTTC	780
ACCNCTCCA	AAGGGGTAT	TCCGGTTTCC	CCNAATCCGG	GGANANCC		828

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTAATT	GCATCCAAAG	TACTAACAAA	AACTCTAGCA	ATCAAGAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACC	TGTGGCTTTT	AAAATTGGT	TTTCATAAGA	TAATTATAC	180
TGAAGTAAAT	CTAGCCATGC	TTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240

ACATTTGGCA TAAACAATAA TAAAACAATC ACAATTAAAT AAATAACAAA TACAACATTG	300
TAGGCCATAA TCATATACAG TATAAGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG	360
AATAGAATAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTTGATTACAC TCAGCCCTGA	420
CATTCAAGTTT TCAAAGTAGG AGACAGGTTAC TACAGTATCA TTTTACAGTT TCCAACACAT	480
TGAAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAAATG CATTACATCC TCAAGAGTTA	540
TCACCAACCC CTCAGTTATA AAAAATTTC AGTTATATT AGTCATATAA CTTGGTGTGC	600
TTATTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAAC AATGGTCCCC TAATGTGATT	660
GATAITGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTGA ACTGGAACAT	720
TGNATNACAG TGTTCCANAG TTNCACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA	780
TGTTATTTTG TTAAAAATTA ATTAAACC TGTTGGAAAA ATAATTGAA ATNA	834

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTT TTTTTTTTTT AAGACCCCTCA TCAATAGATG GAGACATACA GAAATAGTCA	60
AACCACATCT ACAAAATGCC AGTATCAGGC GGCGGCTTCG AAGCCAAAGT GATGTTGGA	120
TGTAAAGTGA AATATTAGTT GGCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT	180
GACGTGAAGT CCGTGGAAAGC CTGTGGCTAC AAAAATGTT GAGCCGTAGA TGCCGTCGGA	240
AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTGTAGG AGGGTAAAT AGAGACCCAG	300
TAAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTCTA TTAGACTATG	360
GTGAGCTCAG GTGATTGATA CTCCTGATGC GAGTAATACG GATGTGTTA GGAGTGGGAC	420
TTCTAGGGGA TTAGCGGGG TGATGCCTGT TGGGGGCCAG TGCCCTCTA GTGGGGGGT	480
AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAATCCT GCGAAGAAAA AAACTTCTGA	540
GGTAATAAAAT AGGATTATCC CGTATCGAAG GCCTTTTG ACAGGTGGTG TGTGGTGGCC	600
TTGGTATGTG CTTTCTCGTG TTACATCGCG CCATCATTGG TATATGGTA GTGTGGTGGG	660
TTANTANGGC CTANTATGAA GAACTTITGG ANTGGATTAA AATCAATNGC TTGGCCGGAA	720
GTCATTANGA NGGCTNAAAA GGCCCTGTAA NGGGTCTGGG CTNGTTTTA CCCNACCCAT	780
GGAATNCNCC CCCCGGACNA NTGNATCCCT ATTCTTAA	818

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 817 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAAATA	60
CGGGCCCTAT TTCAAAGATT TTTAGGGAA TTAATTCTAG GACGATGGGT ATGAAACTGT	120
GGTTTGCTCC ACAGATTCA GAGCATTGAC CGTAGTATAC CCCCGGTGCGT GTAGCGGTGA	180
AAGTGGTTTG GTTTAGACGT CGGGGAATTG CATCTGTTT TAAGCTAAT GTGGGGACAG	240
CTCATGAGTG CAAGACGTCT TGTGATGTAA TTATTATACN AATGGGGCT TCAATCGGGA	300

GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTTCTAGG AATAATGGGG	360
GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT GTTCTCTAG GTCAATACC	420
ATTGGTGGCC AATTGATTG ATGGTAAGGG GAGGGATCGT TGAACTCGTC TGTTATGTA	480
AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA TNAATGGCGG GCANGATATT	540
TCAAACNGTC TCTANTCCT GAAACGTCTG AAATGTTAAT AANAATTAAN TTTNGTTATT	600
GAATNTTNNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNNTAANGG	660
CNTTATCNTR AAAGGTNATA ACCNCTCCTA TNATCCCACC CAATNGNATT CCCCACNCNN	720
ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG TGNANNCCNC CTTTTGTTCC	780
CTTNANTGAN GGTTATTNC CCCTNGCNTR ATCANC	817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG	60
CATAAGGAGA ACTTTCTGCT GGCACCGCGT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT	120
CTGAAGGCCA CGTCCCGAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA CATCCGCGAG	180
TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG CGTCCTGGGG	240
TGGGTGGCCG ANGCGTGAN CGCTCTGCCT TGCTGCCCCC ANGTGGGCCG CCACCCCCCTG	300
ACCTGCCTGG GTCCAAACAC TGAGCCCTGC TGGCGGACTT CAAGGANAAC CCCCACANGG	360
GGATTTGCT CCTANANTAA GGCTCATCTG GGCTCGGCC CCCCACCTG GTTGGCCTTG	420
TCTTGTGAGT GAGCCCCATG TCCATCTGGG CCACTGTCNG GACCACCTT NGGGAGTGT	480
CTCCCTAACAA CCACANNATG CCCGGCTCCT CCCGGAAACC ANTCCCANCC TGNGAAGGAT	540
CAAGNCCTGN ATCCACTNNT NCTANAACCG GCCNCCNCCG CNGTGGAACCC CNCCTTNTGT	600
TCCCTTTCTN TNAGGGTTAA TNNGCCTTG GCCTTNCCAN NGTCCNCNC NTTTCCNN	660
GTINAAATTG TTANGCNCCC NCCNNTCCN CNNCNCCNAN CCCGACCCNN ANNTTNNANN	720
NCCCTGGGGT NCCNNCGAT TGACCCNNCC NCCCTNTANT TGCNTTNGGG NNCNNTGCC	780
CTTCCCTCT NGGGANNNC	799

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCCTTGAT CCTCCCAGGC TGGGACTGGT TCTGGGAGGA GCCGGGCATG CTGTGGTTG	60
TAANGATGAC ACTCCCAAAG GTGGTCCTGA CAGTGGCCCA GATGGACATG GGGCTCACCT	120
CAAGGACAAG GCCACCAGGT CGGGGGCCG AAGCCCACAT GATCCTTAAT CTATGAGCAA	180
AATCCCTGT GGGGGCTTCT CCTTGAAAGTC CGCCANCAGG GCTCAGTCTT TGGACCCANG	240
CAGGTGATGG GGTTGTNGNC CAACTGGGG CCNCAACGCA AAANGCNCA GGGCCTCNGN	300
CACCCATCCC ANGACGCGGC TACACTNCTG GACCTCCCNC TCCACCACTT TCATGCGCTG	360

TTCNTACCCG CGNATNTGTC CCANCTGTT CNGTGCNAC TCCANCTCT NGGACGTGCG	420
CTACATACGC CGGGANTCNC NCTCCGCTT TGTCCTATC CACGTNCCAN CAACAAATT	480
CNCCNTANTG CACCNATTCC CACNTTNNC AGNTTCCNC NNCGNGCTTC CTNTAAAAG	540
GGTGANCCC CGGAAAATNC CCCAAAGGGG GGGGGCCNGG TACCCAACN CCCCCTNATA	600
GCTGAANTCC CCATNACCCN GNCTCNATGG ANCCNTCCNT TTTAANNACN TTCTNAACTT	660
GGGAANANCC CTCGNCCNTN CCCCCNTTAA TCCCNCCNTG CNANGNNCNT CCCCCNNNTCC	720
NCCCNNTNG GCNTNTNANN CNAAAAAGGC CCNNNANCAA TCTCCTNNCN CCTCANTTCG	780
CCANCCCTCG AAATCGGCCN C	801

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT GGCCAGTGTG GCAGCTTICCG CTGTGGCTGC CGGTGCCACA TGCCTGTCCC	60
ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCCTCACCGG GTTCACCTTC TCAGCCCTGC	120
AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCAGGA GAAGCAGGTG TTCTGCCCCA	180
AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACC AGCTTCCCTGC	240
CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT GGGTGCCTGG AAGCAGTGGCC	300
TGCTCCCACC TCCACCCCGCG CTCTGCGGGG CCTCTGCCTG TGATGCTCTCC GTACGTGTGG	360
TGGTGGGTGA GCCCACCGAN GCCAGGGTGG TTCCGGGCGG GGGCATCTGC CTGGACCTCG	420
CCATCCCTGGA TAGTGTTCCTC TGCTGTCCCA NGTGGCCCA TCCCTGTTTA TGGGCTCCAT	480
TGTCCAGCTC AGCCAGTCTG TCACTGCCTA TATGGTGTCT GCCGCAGGCC TGGGTCTGGT	540
CCCATTAACT TTGCTACACA GGTANTATT GACAAGAACG ANTTGGCCAA ATACTCAGCG	600
TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGTCC AACTCCCCGC	660
TCCTGTTAAC CCCATGGGC TGCGGGCTTG GCCGCCAATT TCTGTTGCTG CCAAANTNAT	720
GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG	780
GGNGTTCCC	789

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 772 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC	60
TTTGTAAAT AAATAAGTTA AATATTTAAA TGCCTGTGTC TCTGTGATGG CAACAGAAGG	120
ACCAACAGGGC CACATCCTGA TAAAAGGTAA GAGGGGGGTG GATCAGCAAA AAGACAGTGC	180
TGTGGGCTGA GGGGACCTGG TTCTTGTGTG TTGCCCCCTCA GGACTCTTCC CCTACAAATA	240
ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTCATCC TAGAAACTCC CATGCAAGAG	300
CTACATTAAA CGAAGCTGCA GGTAAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT	360
TATTCAGCTC CCAAAACCC TTCTCTAGGT GTGTCTAAC TAGGAGGCTA GCTGTTAAC	420

CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGAA	AAAAGAAAAG	GACGCCCCAN	CCCCCAGCTG	TGCANCTACG	CACCTCAACA	600
GCACAGGGTG	GCAGCAAAAA	AACCACTTA	CTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGGG	GTAAACAGGA	ANCNGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCAC	CCCNAAATNTT	GCTGGGAAAT	TTTCCTCCC	CTAAATTNTT	TC	772

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATT	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GGAAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGCGACCAC	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TCNCGAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	CCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCNA	AAAATCTTCA	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCACTG	600
CCAACAGGGG	CTGCCCCACN	CNCNNAACGA	TGANCCNATT	GNACAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCTGCGN	TNGTGGCTCC	TGTTICAGGNC	CNNGGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNGGANANN	G			751

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTGTCCCT	60
TGTGGAN CCT	CAGCAGTNCC	CTCTTTAGA	ACTCANTGCC	AAGANCCCTG	AA CAGGAGCC	120
ACCATGCA GT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCAATT	GCTCATCTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTT	240
CTGAAGATCT	TGGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTT	TTCTTCATCC	TCCTCCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAA	GGCTGAGCAC	TTCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCA ACTA	TACGGATT	600

GAAGANTCAC CTACTTCAAA GAAAANAGTG CCTTTCCCCC ATTTCTGTTG CAATTGACAA	660
ACGTCCCCAA CACAGCCAAT TGAAAACCTG CACCCAACCC AAANGGGTCC CCAACCANAA	720
ATTNAAGGG	729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT CAAAGTTGTT CTTGTTGCCA TAACAACCAC CATAGGTAAA GCGGGCGCAG	60
TGTCGCTGA AGGGGTTGTA GTACCAGCGC GGGATGCTCT CCTTGAGAG TCCTGTGTCT	120
GGCAGGTCCA CGCAGTGCCTC TTTGTCAGT GGGAAATGGA TGCGCTGGAG CTCGTCAAAG	180
CCACTCGTGT ATTTCACACA GGCAGCCTCG TCCGACGCGT CGGGGCAGTT GGGGGTGTCT	240
TCACACTCCA GGAAACTGTC NATGCAGCAG CCATTGCTGC AGCGGAACGT GGTGGGCTGA	300
CANGTGCCAG AGCACACTGG ATGGCGCTT TCCATGNNA GGGCCCTGNG GGAAAGTCCC	360
TGANCCCCAN ANCAGCTCT CAAANGCCCC ACCTTGACACA CCCCGACAGG CTAGAATGGA	420
ATCTTCTTCC CGAAAGGTAG TTNTTCTTGT TGCCCAANCC ANCAGCTTAA ACAAACTCTT	480
GCANATCTGC TCCGNGGGGG TCNTANTACC ANCAGTGGAA AAGAACCCCA GGCGNGGAAC	540
CAANCTTGTG TGGATNCGAA GCNATAATCT NCTNTTCTGC TTGGTGGACA GCACCANTNA	600
CTGTNNNACT TTAGNCCNTG GTCCTCNTGG GTTGNNTTG AACCTAATCN CCNNTCAACT	660
GGGACAAGGT AAANTNGCCNT CTTTNAATT CCCNANCNTN CCCCTGGTT TGGGGTTTN	720
CNCNCTCCTA CCCCAGAAAAN NCCGTGTTCC CCCCAACTA GGGGCNAAA CCNNTTNTTC	780
CACAACCCTN CCCCACCCAC GGGTCNGT GGTTNG	816

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG GGCAGGCATA NACTTGAAGG TACAACCCCA GGAACCCCTG GTGCTGAAGG	60
ATGTGGAAA CACAGATTGG CGCCTACTGC GGGGTGACAC GGATGTCAGG TAGAGAGGAA	120
AAGACCCAAA CCAGGTGGAA CTGTGGGAC TCAAGGAANG CACCTACCTG TTCCAGCTGA	180
CAGTGACTAG CTCAGACCCAC CCAGAGGACA CGGCCAACGTT CACAGTCACT GTGCTGTCCA	240
CCAAGCAGAC AGAACGACTAC TGCCTCGCAT CCAACAAANG GGGTCGCTGC CGGGGCTCTT	300
TCCCACGCTG GTACTATGAC CCCACGGAGC AGATCTGCA GAGTTTCGTT TATGGAGGCT	360
GCTTGGCAA CAAGAACAAAC TACCTTCGGG AAGAAGAGTG CATTCTANCC TGTCNGGGTG	420
TGCAAGGTGG GCCTTTGANA NGCANCTCTG GGGCTCANGC GACTTTCCCC CAGGGCCCT	480
CCATGGAAAG GCGCCATCCA NTGTTCTCTG GCACCTGTCA GCCCACCCAG TTCCGCTGCA	540
NCAATGGCTG CTGCATCNAC ANTTCCCTNG AATTGTGACA ACACCCCCCA NTGCCCCCAA	600
CCCTCCCCAAC AAAGCTTCCC TGTNAAAAA TACNCCANTT GGCTTTNAC AACACNCCGG	660
CNCCTCCNTT TTCCCCNNNT AACAAAGGGC NCTNGCNTT GAACTGCCN AACCCNGGAA	720

TCTNCCNNGG AAAAANTNCC CCCCCCTGGTT CCTNNAANCC CCTCCNCNAA ANCTNCCCCC CCC	780 783
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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTC CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTTGGAT GTCATACAAA	60
AGCTGATTGA AGCAACCCCTC TACTTTTG TGCGAGCCT TTTGTTGGT GCAGGTTTCA	120
TTGGCTGTGT TGGTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCACT GTTCTTTG	180
AAGTAGGGTG AGTCCTCAAATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTTC	240
ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGGAAC CATAATCTT CTTGATGGCA	300
GGCACTACCA GCAACGTCAG GAAGTGCTCA GCCATTGTGG TGTACACCAA GGCACCACA	360
GCAGCTGCAA CCTCAGCAAT GAAGATGAGG AGGAGGATGA AGAAGAACGT CNCGAGGGCA	420
CACTTGCTCT CGCTTCTAGC ACCATAGCAG CCCANGAAAC CAAGAGAAA GACCACAACG	480
CCNGCTGCGA ATGAAAGAAA NTACCCACGT TGACAAACTG CATGCCACT GGACGACAGT	540
TGGCCCGAAN ATCTTCAGAA AAGGGATGCC CCATGATTG AACACCCANA TGCCCACGTG	600
CNACAGGGCT GCNCNCNCN GAAAGAATGA GCCATTGAAG AAGGATCNIC NTGGTCTTAA	660
TGAACGTAAA CCNTGCATGG TGGCCCTGT TCAGGGCTCT TGGCAGTGAA TTCTGANAAA	720
AAGGAACNGC NTNAGCCCC CCAAANGANA AAACACCCCCC GGGTGTGCCCC CTGAATTGGC	780
GGCCAAGGAN CCCTGCCCCN G	801

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA GGCGTCCCTC TGCCCTGCCA CTCAGTGGCA ACACCCGGGA GCTGTTTGT	60
CCTTTGTGGA GCCTCAGCAG TTCCCTCTTT CAGAACTCAC TGCCAAGAGC CCTGAACAGG	120
AGCCACCATG CAGTGCTTCA GCTTCATTAA GACCATGATG ATCCTCTTCA ATTGCTCAT	180
CTTCTGTGT GGTGCAGCCC TGTTGGCAGT GGGCATCTGG GTGTCAATCG ATGGGGCATC	240
CTTCTGAAG ATCTTCGGGC CACTGTCGTC CAGTGCCATG CAGTTTGTC ACGTGGGCTA	300
CTTCCTCATC GCAGCCGGCG TTGTGGTCTT TGCTCTTGGT TTCCCTGGCT GCTATGGTGC	360
TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTTCTTC ATCCTCCTCC TCATCTTCAT	420
TGCTGAAGTT GCAGCTGCTG TGGTCGCCCTT GGTGTACACC ACAATGGCTG AACCAATTCC	480
GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAAGGAA AAATTCACTC	540
AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGGCTTCCCC AACTATACCG	600
GAATTTTGAA AGANTCNCCC TACTTCCAAA AAAAAANANT TGCCCTTNCC CCCNTTCTGT	660
TGCAATGAAA ACNTCCCAAN ACNGCCAATN AAAACCTGCC CNNNAAAAA GGNTNCAAA	720
CAAAAAAANT NNAAGGGTTN	740

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG	CGCTGGTCCA	GNGNAGCCAC	GAAGCACGTC	AGCATAACACA	GCCTCAATCA	60
CAAGGTCTTC	CAGCTGCCGC	ACATTACGCA	GGGCAAGAGC	CTCCAGCAAC	ACTGCATATG	120
GGATACACTT	TACTTTAGCA	GCCAGGGTGA	CAACTGAGAG	GTGTCGAAGC	TTATTCTTCT	180
GAGCCTCTGT	TAGTGGAGGA	AGATTCCGGG	CTTCAGCTAA	GTAGTCAGCG	TATGTCCCCT	240
AAGCAAACAC	TGTGAGCAGC	CGGAAGGTAG	AGGCAAAGTC	ACTCTCAGCC	AGCTCTCTAA	300
CATTGGCAT	GTCCAGCAGT	TCTCCAAACA	CGTAGACACC	AGNGGCCTCC	AGCACCTGAT	360
GGATGAGTGT	GGCCAGCGCT	GCCCCCTTGG	CCGACTTGCG	TAGGAGCAGA	AATTGCTCCT	420
GGTTCTGCC	TGTCACCTTC	ACTTCCGCAC	TCATCACTGC	ACTGAGTGTG	GGGGACTTGG	480
GCTCAGGATG	TCCAGAGACG	TGGTTCCGCC	CCCTCNCTTA	ATGACACCGN	CCANNCAACC	540
GTCGGCTCCC	GCCGANTGNG	TTCGTCGTNC	CTGGGTCAGG	GTCTGCTGGC	CNCTACTTGC	600
AANCTTCGTC	NGGCCCATGG	AATTCAACNC	ACCGGAACTN	GTANGATCCA	CTNNNTCTAT	660
AACCGGNCGC	CACCGCNNT	GGAACTCCAC	TCTTNTINCC	TTTACTTGAG	GGTTAACGGTC	720
ACCCCTNNCG	TTACCTTGGT	CCAAACCNNT	CCNTGTGTCG	ANATNGTNAA	TCNGGNCCNA	780
TNCCANCCNC	ATANGAAGCC	NG				802

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC	AGGTNACGGG	CCGCNAANCC	TGACCCNAGG	TANCANAANG	CAGNCNGCGG	60
GAGCCCACCG	TCACGNNGNG	GNGTCTTTAT	NGGAGGGGGC	GGAGCCACAT	CNCTGGACNT	120
CNTGACCCCA	ACTCCCCNCC	NCNCANTGCA	GTGATGAGTG	CAGAACTGAA	GGTNACGTGG	180
CAGGAACCAA	GANCAAANNC	TGCTCCNNTC	CAAGTCGGCN	NAGGGGGCGG	GGCTGGCCAC	240
GCNCATCCNT	CNAGTGTGN	AAAGCCCCNN	CCTGTCTACT	TGTTTGGAGA	ACNGCENNNA	300
CATGCCAGN	GTTANATAAC	NGGCNGAGAG	TNANTTTGCC	TCTCCCTTCC	GGCTGCGCAN	360
CGNGNTGCT	TAGNGGACAT	AACCTGACTA	CTTAACTGAA	CCCNNGAATC	TNCCNCCCC	420
CCACTAAGCT	CAGAACAAA	AACTTCGACA	CCACTCANTT	GTCACCTGNC	TGCTCAAGTA	480
AAGTGTACCC	CATNCCCAAT	GTNTGCTNGA	NGCTCTGNCC	TGCNTTANGT	TCGGTCCTGG	540
GAAGACCTAT	CAATTNAAGC	TATGTTTCTG	ACTGCCTCTT	GCTCCCTGNA	ACAANCNACC	600
CNNCNNTCCA	AGGGGGGGNC	GGCCCCAAT	CCCCCAACC	NTNAATTNAN	TTTANCCCN	660
CCCCCNGGCC	CGGCCTTTA	CNANCNTCNN	NNACNGGGNA	AAACCNNGC	TTTNCCCAAC	720
NNAATCCNCC	T					731

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTTT TTTTTTTTTT TAAAAACCCC CTCCATTNAA TGNAACCTTC CGAAATTGTC	60
CAACCCCCCTC NTCAAATNN CCNTTCCGG GNNGGGGTTTC CAAACCCAAN TTANNTTTGG	120
ANNTTAAATT AAATNTTNNT TGGNGNNNA ANCCNAATGT NANGAAAGTT NAACCCANTA	180
TNANCTTNAA TNCCCTGGAAA CCNGTNGNTT CCAAAAAATNT TTAACCCCTTA ANTCCCTCCG	240
AAATNGTTNA NGGAAAACCC AANTTCTCNT AAGGTTGTTT GAAGGNTNAA TNAAAANCCC	300
NNCCAATTGT TTTTNGCCAC GCCTGAATTA ATTGGNTTCC GNTGTTTCC NTTAAAANAA	360
GGNNANCCCC GGTTANTNAA TCCCCCNNC CCCAATTATA CCGANTTTT TTNGAATTGG	420
GANCCCNCGG GAATTAACGG GGNNNNNTCCC TNTTGGGGGG CNNGNNCCCC CCCCNCTCGGG	480
GGTTNGGGNC AGGNCCNAAT TGTTTAAGGG TCCGAAAAAT CCCTCCNAGA AAAAAANCTC	540
CCAGGNTGAG NNTNGGGTTT NCCCCCCCCC CANGGCCCT CTCGNANAGT TGGGGTTTGG	600
GGGGCCTGGG ATTTNTTTC CCCTNTTNCC TCCCCCCCCC CNNGGANAG AGGTTNGNGT	660
TTTGNTCNNC GGCCCCNCCN AAGANCTTN CCGANTTNAN TTAAATCCNT GCCTNGGCAGA	720
AGTCCNTIGN AGGGNTAAAN GGCCCCCTNN CGGG	754

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT GACCCCNAAC NNNGGACCNC TCANCCGGNC NNNCNACCNC CGGCCNATCA	60
NNGTNAGNNC ACTNCNNTTN NATCACNCCC CNCCNACTAC GCCCNANC CNACGCNCTA	120
NNCANATNCC ACTGANNGCG CGANGTNGAN NGAGAAANCT NATACCANAG NCACCCANACN	180
CCAGCTGTCC NANAANGCCT NNNATACNGG NNNATCCAAT NTGNANCCTC CNAAGTATTN	240
NNCNNCANAT GATTTTCCTN ANCCGATTAC CCNTNCCCCC TANCCCTCC CCCCCAACNA	300
CGAAGGCNCT GGNCCNAAGG NNGCGNCNCC CCGCTAGNTC CCCNNCAAGT CNNCNCNCTA	360
AACTCANCCN NATTACNGC TTCNTGAGTA TCACTCCCCG AATCTCACCC TACTCAACTC	420
AAAANATCN GATACAAAAT AATNCAAGCC TGNTTATNAC ACTNTGACTG GGTCCTATT	480
TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCT TCNCCAATT CCNAANGGCT	540
CTTTCNGACA GCATNTTTG GTTCCCNNTT GGGTTCTTAN NGAATTGCC TTCTNTGAAC	600
GGGCTCNTCT TTTCCTTCGG TTANCTGGN TTCNNCCGGC CAGTTATTAT TTCCCNNTTT	660
AAATTCTNCC CNTTANTTT TGGCCTTCNA AACCCCCGGC CTTGAAAACG GCCCCCTGGT	720
AAAAGGTTGT TTTGANAAAA TTTTGTGTTT GTTCC	755

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTT	TTTTTANGTG	TNGTCGTGCA	GGTAGAGGCT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGACC	CGANTTCTAG	GANNCCNCCCT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNNA	CGGAANGGTC	ACCGGNNGAT	NNTGCTAGGG	TGNCCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCC	CACCACCTTC	GGCGGCCNG	NGNCCGGGC	CGGGTCATTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTTCCN	NCCCCNNCNG	ACCCNGGC	TCCCCGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAANTGGG	CCNCGGNCCC	CTTTACCCCT	NNACAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCCTCCANT	NNGGGGACT	GCCNANNGCT	CCGTTNCTNG	420
NNACCCCN	GGGTNCCTCG	GTGTCGANT	CNAACGNANG	CCANGGATT	CNAAGGAAGG	480
TGCGTTNTTG	GCCCCTACCC	TCGCTNCGG	NNCACCCCTTC	CCGACNANGA	NCCGCTCCCG	540
CNCNCNGNNG	CCTCNCCCTCG	CAACACCCGC	NCTCNTCNGT	NCGGNNNCCC	CCCCACCCGC	600
NCCCTCNCNC	NGNGNANCN	CTCCNCCNCC	GTCTCANNCA	CCACCCCGCC	CCGCCAGGCC	660
NTCANCCACN	GGNNGACNNG	NAGCNCNNTC	GCNCAGCGCN	GCGNCNCCT	CGCCNCNGAA	720
CTNCNTCNGG	CCANTNNCGC	TCAANCCNA	CNAACGCCG	CTGCGGGCC	CGNAGCGNCC	780
NCCTCCNCGA	GTCCTCCGN	CTTCNACCC	ANGNNTTCCN	CGAGGACACN	NNACCCCGCC	840
NNCANGCGG						849

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAACTA	TACTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTCCCTC	CGCAACCATG	60
TCTGACNANC	CCGATTNGGC	NGATATCNAN	AAGNTCGANC	AGTCCAAACT	GANTAACACA	120
CACACNCNAN	AGANAAATCC	NCTGCCTTCC	ANAGTANACN	ATTGAACNNG	AGAACCAANGC	180
NGGCGAATCG	TAATNAGGCG	TGCGCCGCCA	ATNTGTCNCC	GTTTATTNTN	CCAGCNTCNC	240
CTNCCNACCC	TACNTCTTCN	NAGCTGTCNN	ACCCCTNGTN	CGNACCCCC	NAGGTGGGA	300
TCGGGTTTNN	NNTGACCGNG	CNNCCCTCC	CCCCNTCCAT	NACGANCCNC	CCGCCACCACC	360
NANNGCNGC	NCCCCGNCT	CTTCGCCNCC	CTGTCCCTNT	CCCCTGTNGC	CTGGCNCNGN	420
ACCGCATTGA	CCCTCGCCNN	CTNCNNGAAA	NCGNANACGT	CCGGGTTGNN	ANNANCCTG	480
TGGGNNNGCG	TCTGCNCCCG	GTTCTTCCN	NCNNCTTCCA	CCATCTTCNT	TACNGGTCT	540
CCNCGCCNTC	TCNNNCACNC	CCTGGGACGC	TNTCCTNTGC	CCCCCTTNAC	TCCCCCCCCTT	600
CGNCGTGNCC	CGNCCCCACC	NTCATTTNCA	NACGNTCTTC	ACAANNNCCT	GGNTNNCTCC	660
CNANCNGNCN	GTCANCCNAG	GGAAAGGGNGG	GGNNCCNNTG	NTTGACGTTG	NGGGNGANGTC	720
CGAANANTCC	TCNCNTCANC	CNCTACCCCT	CGGGCGNNCT	CTCNGTNCC	AACTTANCAA	780
NTCTCCCCCG	NGNGCNCNTC	TCAGGCTCNC	CCNCCCCNCT	CTCTGCANTG	TNCTCTGCTC	840
TNACCNNTAC	GANTNTTCGN	CNCCCTCTTT	CC			872

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC TTGAGTATTC TATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA	60
NCTGNCTTCC TGTGTCAAAT GTATAACNAAN TANATATGAA TCTNATNTGA CAAGANNGTA	120
TCNTNCATTA GTAACAANTG TNNTGTCCAT CCTGTCNGAN CANATTCCCA TNNATTNCGN	180
CGCATTNCNC GCNCANTATN TAATNGGGAA NTCNNNTNNN NCACCNNCAT CTATCNTNCC	240
GCNCCTGAC TGGNAGAGAT GGATNANTTC TNNTNTGACC NACATGTTCA TCTTGGATTN	300
AANANCCCCC CGCNGNCCAC CGGTTNGNNG CNAGCCNNTC CCAAGACCTC CTGTGGAGGT	360
AACCTGCGTC AGANNCATCA AACNTGGAA ACCCGCNCC ANGTNNAAGT NGNNNCANAN	420
GATCCCCTGCC AGGNTTNACC ATCCCTTCNC AGCGCCCCCT TTNGTGCTT ANAGNGNAGC	480
GTGTCCNANC CNCTCAACAT GANACGCGCC AGNCCANCCG CAATTNGGCA CAATGTCGNC	540
GAACCCCCCTA GGGGGANTNA TNCAAANCCC CAGGATTGTC CNCNCANGAA ATCCCNCANC	600
CCCNCCCTAC CCNNCTTGG GACNGTGACC AANTCCCGGA GTNCCAGTCC GCCNGNCTC	660
CCCCACCGGT NNCCNTGGGG GGGTGAANCT CNGNNTCANC CNGNCGAGGN NTCGNAAGGA	720
ACCGGNCCTN GGNCGAANNG ANCNCNTCNGA AGNGCCNCNT CGTATAACCC CCCCTCNCCA	780
NCCNACNGNT AGNTCCCCCCC CNGGGTNCGG AANGG	815

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC TCGCTCCGTG GCCTTAGCTG TGCTCGCGCT ACTCTCTCTT TCTGGCCTGG	60
AGGCTATCCA GCGTACTCCA AAGATTCAAGG TTTACTCAGC TCATCCAGCA GAGAATGGAA	120
AGTCAAATTT CCTGAATTGC TATGTGTCTG GGTTTCATCC ATCCGACATT GAANTTGACT	180
TACTGAAGAA TGGANAGAGA ATTAAAAAG TGGAGCATTC AGACTTGTCT TTCAGCAAGG	240
ACTGGTCTTT CTATCTCNG TACTACACTG AATTCAACCC CACTGAAAAA GATGAGTATG	300
CCTGCCGTGT GAACCATGTG ACTTTGTAC AGCCCAAGAT AGTTAAGTGG GATCGAGACA	360
TGTAAGCAGN CNNCATGGAA GTTTGAAGAT GCGCATTG GATTGGATGA ATTCAAATT	420
CTGCTTGCTT GCNTTTAAT ANTGATATGC NTATACACCC TACCCTTAT GNCCCCAAAT	480
TGTAGGGTT ACATNANTGT TCNCNTNGGA CATGATCTTC CTTTATAANT CCNCNTTCG	540
AATTGCCGT CNCCNGTT NGAATGTTTC CNNAACCACG GTTGGCTCCC CCAGGTCNCC	600
TCTTACGGAA GGGCCTGGGC CNCTTNCAA GTTGGGGGA ACCNAAAATT TCNCTNTGC	660
CCNCCCNCCA CNNTCTTNGN NNCNCANTTT GGAACCCCTC CNATTCCCT TGGCCTCNNA	720
NCCTTNCTA ANAAACTTN AAACGTNGC NAAANNTTN ACTTCCCCCC TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC AGTGTAATCT TTTCCCAGAG GTGTGTANAG GGAACGGGGC CTAGAGGCAT	60
CCCANAGATA NCTTATANCA ACAGTGCTTT GACCAAGAGC TGCTGGGCAC ATTCCCTGCA	120
GAAAAGGTGG CGGTCCCCAT CACTCCTCCT CTCCCATAGC CATCCAGAG GGGTGAGTAG	180
CCATCANGCC TTCGGTGGGA GGGAGTCANG GAAACAACAN ACCACAGAGC ANACAGACCA	240
NTGATGACCA TGGGCGGGAG CGAGCCTCTT CCCTGNACCG GGGTGGCANA NGANAGCCTA	300
NCTGAGGGGT CACACTATAA ACGTTAACGA CCNAGATNAN CACCTGCTTC AAGTGCACCC	360
TTCCCTACCTG ACNACCAGNG ACCNNNAACT GCNGCCTGGG GACAGCNCTG GGANCAGCTA	420
ACNNAGCACT CACCTGCCCT CCCATGGCCG TNCGCNTCCC TGGTCCTGNC AAGGGAAGCT	480
CCCTGTTGGA ATTNCGGGA NACCAAGGGA NCCCCCTCCT CCANCTGTGA AGGAAAAANN	540
GATGGAATTG TNCCCTTCCG GCCNNNTCCC TCTTCCTTTA CACGCCCTT NNTACTCN	600
TCCCTCTNTT NTCCCTGNNC ACTTTTNACC CCNNNATTTC CCTTNATTGA TC GGANNCTN	660
GANATTCCAC TNNGCCTNC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGAT	720
GGGNNCTCG NTCATCCTCT CTTTTCNCT ACCNCCNNTT CTTTGCCTCT CCTTNGATCA	780
TCCAACCNTC GNTGGCCNTN CCCCCCNNTN TCCTTTNCCC	820

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT GGCCTCTTCC TCCTCAGGGA CCTCTGACTG CTCTGGGCCA AAGAATCTCT	60
TGTTTCTTCT CCGAGCCCCA GGCAGCGGTG ATTTCAGCCCT GCCAACCTG ATTCTGATGA	120
CTGCGGATGC TGTGACGGAC CCAAGGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGGGCGC	180
CTGCTGAGCA CTTCCGCCCT TCACCCCTGCC CAGCCCCCTGC CATGAGCTCT GGGCTGGGTC	240
TCCGCCTCCA GGGTTCTGCT CTTCCANGCA NGCCANCAAG TGGCGCTGGG CCACACTGGC	300
TTCTTCCTGC CCCNTCCCTG GCTCTGANTC TCTGTCTTCC TGTCTGTGC ANGCNCCTTG	360
GATCTCAGTT TCCCTCNCTC ANNGAACTCT GTTTCTGANN TCTTCANTTA ACTNTGANTT	420
TATNACCNA TGGNCTGTNC TGTCNNACTT TAATGGGCCN GACCGGCTAA TCCCTCCCTC	480
NCTCCCTTCC ANTCNNNA ACCNGCTTNC CNTCNCTCC CCNTANCCCG CCNGGGAAANC	540
CTCCTTTGCC CTNACCANGG GCCNNNACCG CCCNTNNCTN GGGGGGCNNG GTNNCTNCNC	600
CTGNTNNCCCN CNCTCNCCNT TNCCTCGTCC CNNCNNGCN NNGCANNTTC NCNGTCCNN	660
TNNCTCTTCN NGNTCGNA NGNTCNCTN TNNNNNGNCN NGNTNNNTNCN TCCCTCTCNC	720
CNNNTGNANG TNNTTNNNNC NCNGNNCCCC NNNNCNNNNN NGGNNTNNN TCTNCNCNGC	780
CCCNCCCCC NGNATTAAGG CCTCCNNCTC CGGGCCNC	818

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 731 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG GAGGGATATT GTANGGGATT GAGGGATAGG AGNATAANGG GGGAGGTGTG	60
TCCAACATG ANGGTGNNGT TCTCTTTGA ANGAGGGTTG NGTTTTTANN CCNGGTGGGT	120
GATTNAACCC CATTGTATGG AGNNAAGGN TTNAGGGAT TTTTCGGCTC TTATCAGTAT	180
NTANATTCCCT GTNAATCGGA AAATNATNTT TCNNCNGAA AATNTTGCTC CCATCCGNAA	240
ATTNCTCCCG GGTAGTCAT NTTNGGGGN CNGCCANGTT TCCCAGGCTG CTANAATCGT	300
ACTAAAGNTT NAAGTGGGAN TNCAAATGAA AACCTNNAC AGAGNATCCN TACCCGACTG	360
TNNNTTNCCT TCGCCCTNTG ACTCTGCNNG AGCCAATAC CCNNGNGNAT GTCNCCNGN	420
NNNGCGNCNC TGAAANNNNC TCGNGGCTNN GANCATCANG GGGTTTCGCA TAAAAGCNN	480
CGTTTCNCAT NAAGGCACCT TNGCCTCATC CAACCCTNG CCCTCNCCA TTTNGCCGTC	540
NGGTTCNCCCT ACGCTNNTNG CNCCCTNNNTN GANATTTNC CCGCCTNGGG NAANCCTCCT	600
GNAATGGGTA GGGNCTTNTC TTTNACCNN GNGGTNTACT AATCNNTNC ACCCCTNCTT	660
TCTCNACCCCC CCCCTTTTT CAATCCCANC GGCNAATGGG GTCTCCCCNN CGANGGGGG	720
NNNCCCANNC C	731

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGNCNC TTCTATGANT ANTNTTAGAT	60
CGCTCANACC TCACANCCTC CCNACNANGC CTATAANGAA NANNAATAGA NCTGTNCNN	120
ATNTNTACNC TCATANNCTT CNNNACCCAC TCCCTTTAA CCCNTACTGT GCCTATNGCN	180
TNCTANTCT NTGCCGCCTN CNANCCACCN GTGGGCCNAC CNCNNGNATT CTCNATCTCC	240
TCNCCATNTN GCCTANANTA NGTNCATACC CTATACCTAC NCCAATGCTA NNNCTAANCN	300
TCCATNANTT ANNNTAACCA CCACTGACNT NGACTTTCNC ATNANCTCCT AATTGAAATC	360
TACTCTGACT CCCACNGCCT ANNNATTAGC ANCNTCCCCC NACNATNTCT CAACCAAATC	420
NTCAACAACC TATCTANCTG TTCNCCAACC NTTNCCTCCG ATCCCCNNAC AACCCCCCTC	480
CCAAATACCC NCCACCTGAC NCCTAACCN CACCATCCCC GCAAGCCNAN GGNCTTTAN	540
CCACTGGAAT CACNATNGGA NAAAAAAAAC CCNAACTCTC TANCNNAT CTCCCTAANA	600
AATNCTCCTN NAATTTACTN NCANTNCCAT CAANCCACN TGAAACNNAA CCCCTGTTTT	660
TANATCCCTT CTTTCGAAAA CCNACCCCTT ANNNCCCAAC CTTTNGGGCC CCCCCNCTNC	720
CCNAATGAAG GNCNCCAAAT CNANGAAAAG NCCNTGAAAA ANCNAAGGCNA ANANNNTCCG	780
CANATCCTAT CCCTTANTTN GGGGNCCCTT NCCCNNGGGCC CC	822

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCTT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCTT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTCGCCA	GCCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCCGTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGCTTTTGT	420
TCCCNTTAAT	GAAGGTTAAT	TGNCNGCTTG	GCGTAATCAT	NGGTCANAAC	TNTTCCCTGT	480
GTGAAATTGT	TTNTCCCTC	NCNATTCCNC	NCNACATACN	AACCCGGAAN	CATAAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTCCN	TTCNGGAAAA	CTGTCNTCCC	CTGCNTNNNT	GAATCGGCCA	CCCCCCNGGG	660
AAAAGCGGTT	TGCNTTTTNG	GGGGNTCCCT	CCNCTTCCCC	CCTCNCTAAN	CCCTNCGCCT	720
CGGTGTTNC	NGGTNGCGGG	GAANGGGNAT	NNNCTCCNC	NAAGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT	TTTTTTTGGC	GATGCTACTG	TTTAATTGCA	GGAGGGGGGG	GTGTGTGTAC	60
CATGTACCAAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGGCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCCAGGGG	TGGGAGCACT	ACANGGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNCACANATC	CCTACGATTG	TTGACACCTG	GATTTCACCA	300
GGGGACCTTC	TGTTCTCCCA	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTTCTT	360
CNGCANTTCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCCNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GCCCCACCTCT	CCCNTCNAAN	AAGTAATTCA	CCCCCCCCCN	CCNTCTNTTG	480
CCTGGGCCCT	TAANTACCCA	CACCGGAAC	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCN	CCTGAANGCG	CCAAGTTGAA	AGGCCACGCC	GTNCCCNCTC	CCCATAGNAN	600
NTTTTNNCNI	CANCTAATGC	CCCCCCNGGC	AACNATCCAA	TCCCCCCCCN	TGGGGGGCCCC	660
AGCCCANGGC	CCCCGNCTCG	GGNNNCCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCAGGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNNCNAC	780
CTCGCCCCCCC	CCNNCGNNG					799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTNCCNAG	GGCAGGTTTA	TTGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGCG	GCGGCGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTNN	AATTCCACG	GGCACAAATGC	GGTCGCANCC	CCTCACCACC	300
NATTAGGAAT	AGTGGTNTTA	CCCNCCNCCG	TTGGCNCACT	CCCCNTGGAA	ACCACTTNTC	360
GCGGCTCCGG	CATCTGGTCT	TAAACCTTGC	AAACNCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	AAAAAAANCN	CCCCAAAACC	480
GNNCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCN	AAAAAAANCT	CCGGGGGGNC	CCAGTTCAA	CAAAGTCATC	600
CCCCTTGGCC	CCCAAATCCT	CCCCCCGNTT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCC	NNGNNAACGNC	TANCAANGNA	TCCCTTTTT	TANAAACGGG	780
CCCCCCNCG						789

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GAECTAAAGTC	TGATGAACTT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAGTTTGC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTTGAGGA	GGTTGTTCAT	CATGATCACA	300
ACAANGAACG	GGGCTCGTT	ATCACCCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCA	GCCATCCCTT	CTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTTT	GTGAGGGTTA	ATTGCGCGCT		480
TGGCGTAATC	ATGGTCATAN	CTGTTTCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCCGGAAGC	ATNAAATTTT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTTCC	AGTCCGGAAA	ACCTGTCCCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTG	CTTNTGGGG	720
CGCNCTTCCC	GCTTTCTCGC	TTCCTGAANT	CCTTCCCCCC	GGTCTTTCGG	CTTGCAGCNA	780
ACGGTATCNA	CCT					793

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGG	ACCGTAAAG	CCCCAATCTT	60
ANCAAGTGCG	GGGAANAGCT	GGGTGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAAACAG	CAGCTAATT	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CCTTCGAGCG	CTACATGGCC	240
CAGCTCAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTCTGG	GCCTCAACCT	CCTCTTCTG	CTGTCCAGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCAANGA	CATACANACC	AATGTCTACA	TCNACCACCA	420
GTGTCTGG	GCAATACTGA	TGGANGGCAG	CTACCNAAA	GTNTTCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTCNCTGA	AGGCCCCCGG	600
ATNCNCTAGT	NCTAGAACATCG	GCCCCGCCATC	GGGGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTN	CCTGTGTTGA	720
AATTNTTAAC	CCCCCACAAAT	TCCACGCCNA	CATTNG			756

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTCGGCT	GCTGTNTTA	AGTTGCTCAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTTGGG	AAAAAAACAN	CAGGATNTGA	GTCTTGATTT	CACCTCCAAT	180
AATCTTCNGG	GCTGTCTGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGACCTC	CCCTTCAAG	TTGTTCCGGC	CTTCATCAAA	300
CTTCTNNAAAN	ANGANNANCC	CANCTTTGTC	GAGCTGGNAT	TTGGANAAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TCGCCTCTGC	TGCCTGCAA	AAACTTGCTT	420
GGCNCAAATC	CGACTCCCCN	TCCTTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCNNTCCNNG	CAGGGTTGGT	GGCANNCCGG	GCCCCNTGCGC	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTGGGGG	600
GGAAANCCGTC	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCNT	660
ACNTNCTGGG	CCGGGTTCAA	ANTCCCTCCN	TTGNCNNNTCN	CCTCGGGCCA	TTCTGGATTT	720
NCCNAACTTT	TTCCCTTCCCC	CNCCCCNCGG	NGTTTGGNTT	TTTCATNGGG	CCCCAACTCT	780
GCTNTTGGCC	ANTCCCCTGG	GGGCNTNTAN	CNCCCCCTNT	GGTCCCNTNG	GGCC	834

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGCGC	CCC GTTCCA	TGACNAAGGC	TCC CTCANG	TTAAATAACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGC CTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCTGTA	180
GGAAAGGCCT	GCCTTGTAAG	ACACCAAAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTACT	240
AATGGAAAAA	AAAATAAAC	AAANAGGTTT	GTTCTCATGG	CTGCCACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTTGCTTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTICAC	CCAGCTGGC	NCCCTTCCCC	CATNTTTGTC	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTNCAGTG	GATCTGCCA	ANANTACCCN	TATCATCNNT	GAATAAAAAG	540
GCCCCTGAAC	GANATGCTTC	CANCANCCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAG	GAATGTTCT	GGGTCCANT	CCCTCCTTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCAAN	TGANATCCCC	NGAAGCACCC	TNCCCTGGC	720
ATTTGANTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 760 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAA	GTTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGTT	CGCTGAAGGG	GTTGTAGTAC	CAGCGCGGG	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTG	TCACTGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTAC	ACTCCACTAA	ACTGTCGATN	CANCAGCCC	TTGCTGCAGC	GGAACTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTCCA	TGGAAGGGCC	TGGGGGAAAT	360
CNCCTNANCC	CAAATGCT	CTCAAAGGCC	ACCTTGACACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGAAAATC	TGCTCCGTGG	GGGTCA TNNN	TACCANGTT	GGGGAAAANAA	ACCCGGCNGN	540
GANCCNCCTT	GTTTGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTAAACNTTG	GGCCGNGTTC	CNCTNGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAA	GGTANGTGCC	TTCCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNTT	720
CTCCTCTNCC	CTAAAATCG	TNTTCCCCCC	CCNTANGGCG			760

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTAAAAAA	CCCCCTCCAT	TGAATGAAAA	60
CTTCCNAAT	TGTCCAACCC	CCTCNCCAA	ATNNCCATT	CGGGGGGGGG	GTTCCAAACC	120

CAAATTAATT TTGGANTTTA AATTAAATNT TNATTNGGG AANAANCAA ATGTNAAGAA	180
AATTAAACCC ATTATNAACT TAAAATNCCTN GAAACCCNTG GNTTCCAAAATTTTAACC	240
CTTAATCCC TCCGAATTG NTAANGAAA ACCAAATTCTN CCTAAGGCTN TTTGAAGGTT	300
NGATTTAAC CCCCTTNANT TNTTTTNACC CNNGNCTNAA NTATTTNGNT TCCGGTGT	360
TCCTNTTAAN CNTNGGTAAC TCCCNTAAT GAANNNCCT AANCCAATTA AACCGAATT	420
TTTTGAATT GGAAATTCCN NGGAATTNA CGGGGGTTT TCCCNTTGG GGGCATNCC	480
CCCNCTTCG GGGTTGGGN NTAGGGTGA TTTTNNANG NCCCCAAAAA NCCCCAANA	540
AAAAAACTCC CAAGNNTAA TTNGAATNTC CCCCTTCCCA GGCCTTTGG GAAAGGNGGG	600
TTNTGGGG CCNNGGANTT CNTTCCCCN TTNCCNCCCC CCCCCCNNGT AAANGTTAT	660
NGNNTTGTT TTTTGGGCC CTTNANGGAC CTTCCGGATN GAAATTAAT CCCGGGNCG	720
GCCG	724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT TTTTTCTTTG CTCACATTAA ATTITATTT TGATTTTTT TAATGCTGCA	60
CAACACAATA TTTATTTCAT TTGTTCTTT TATTCATTT TATTGTTTG CTGCTGCTGT	120
TTTATTTATT TTTACTGAAA GTGAGAGGGA ACTTTGTGG CCTTTTTCC TTTTCTGTA	180
GGCCGCCCTTA AGCTTTCTAA ATTTGGAACA TCTAAGCAAG CTGAANGGAA AAGGGGGTTT	240
CGCAAAATCA CTCGGGGGAA NGGAAAGGTT GCTTGTAA TCATGCCCTA TGGTGGGTGA	300
TTAAGCTGCTT GTACAATTAC NTTTCACTTT TAATTAATTG TGCTNAANG TTTAATTANA	360
CTTGGGGGTT CCCTCCCCN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG	420
TCCCGGCNT CNTGAAACA CACNGNGAA NGTTCTCATT NTCCCCNCNC CAGGTNAAA	480
TGAAGGGTTA CCATNTTAA CNCCACCTCC ACNTGGCENN GCCTGAATCC TCNAAAANCN	540
CCCTCAANCN AATTNCTNNG CCCCAGTCNC GCNTNNGTCC CNCCCGGGCT CGGGGAANTN	600
CACCCCNNGA ANNCNTNNNC NAACNAAATT CCGAAAATAT TCCCNNTCNC TCAATTCCCC	660
CNNAGACTNT CCTCNCNAN CNCAATTTC TTTTNNTCAC GAACNCGNNC CNNAAAATGN	720
NNNNNCNCCTC CNCTNGTCCN NAATCNCCAN C	751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTTT CTGTAAGATC AGGTGTTCCCT CCCTCGTAGG TTTAGAGGAA ACACCCTCAT	60
AGATGAAAAC CCCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGG GTAGGGAGGG	120
CGCCCTATGC ACAGCTGGGC CCTTGAGACA GCAGGGCTTC GATGTAGGC TCGATGTCAA	180
TGGTCTGGAA CGGGCGGCTG TACCTGCGTA GGGGCACACC GTCAGGGCCC ACCAGGAACT	240
TCTCAAAGTT CCAGGCAACN TCGTTGCGAC ACACCGGAGA CCAGGTGATN AGCTTGGGT	300

CGGTATAAN CGCGGTGGCG TCGTCGCTGG GAGCTGGCAG GGCTCCCGC AGGAAGGCNA	360
ATAAAAGGTG CGCCCCCGCA CCGTTCANCT CGCACTTCTC NAANACCATG ANGTTGGGCT	420
CNAACCCACC ACCANNCCGG ACTTCCTTGA NGGAATTCCC AAATCTCTC GNTCTTGGC	480
TTCTNCTGAT GCCCTANCTG GTTGCCNGN ATGCCAANCA NCCCCAANCC CGGGGGTCT	540
AAANCACCCN CCTCCTCNNT TCATCTGGT TTTNTCCCC GGACCNNTGGT TCCTCTCAAG	600
GGANCCATA TCTCNACCAN TACTCACCN NCCCCCCNT GNNACCCANC CTTCTANNGN	660
TTCCCNCCCG NCCTCTGGCC CNTCAAANAN GCTTNCACNA CCTGGGTCTG CCTTCCCCCC	720
TNCCCTATCT GNACCCCN CN TTTGTCTCAN TNT	753

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA TCACAACAGA CATGCTTCAT CCCATAGACT TCTTGACATA GCTTCAAATG	60
AGTGAACCCA TCCTTGATTT ATATAACATAT ATGTTCTCAG TATTTTGGA GCCTTCCAC	120
TTCTTAAAC CTTGTTCATT ATGAACACTG AAAATAGGAA TTTGTGAAGA GTTAAAAAGT	180
TATAGCTTGT TTACGTAGTA AGTTTTGAA GTCTACATTC AATCCAGACA CTTAGTTGAG	240
TGTTAAACTG TGATTTTAA AAAATATCAT TTGAGAATAT TCTTTCAGAG GTATTTCAT	300
TTTACTTT TGATTAATTG TGTTTATAT ATTAGGGTAG T	341

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA TTTAGTTCTG TGCTCTTCCT TATTTAGTGT TGTATCATAA ATACTTGAT	60
GTTTCAAACA TTCTAAATAA ATAATTTCA GTGGCTTCAT A	101

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTCCTG GTCCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAAACCCA	180
CCTCTTGAGA GGTCAGTAA GAGGACTTAA TATTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTTTGTGTTCT	60
GATTATTTGG TGTGTGTTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTC	120
CTCTCCATCC TCGGGCATTC TTCCCCAAATT TATATACCAAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTC TCTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTCA TAGGTCATGC	240
TGCTGTTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTAA TTAATCCTGG GTTCTTGCTC GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGTTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCCCGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTCA TATAAAATAGT TCTNGTCTTT CCAGGGTTC ATGATGGAAG	600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC	660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCCGTCCCTG	720
CCGCCCGGGT GAACTCCTGC AAACCTCATGC TCCAAAGGTG CTCGCCGTG ATGTCGAAC	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GTTGGTGTCA CAGGAGGTGA TGGAGCCACT	840
CCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG	180
TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGTTAAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTTCA AAANAAAANAA TTATTGCACT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAAN AACTGAAGGG CANAAAGAAAT TAATTTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GGTTCAAGAC	120

GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCCAA	240
AACATCAAAG AAAGGAAGGT GGCGTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGA CAACTGACCA TGTCCCCAGG CCTCTGTGTG	360
CTGGCTCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC	420
CCACACTCCT TGAACACACA TCCCCAGGTT ATATTCCCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTCCG AGATGCCCTG CTCCCTGCAG CCTGTCAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTTCT GACTTGCGCTG ATTACTCCAG CATCTTGGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACCAGCTATG GGACCTTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNTCATT TTGTTCTACC TGAAAATGG GGGATAATAA TAGT	774

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCCCTT AATTACAGCT CAACGCAACT	120
TGGT	124

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCCAA GCANTGT	147

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAATT AATAAAAGGA CTGTTGGGT TCTGCTAAA CACATGGCTT GATATATTGC	60
ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT	107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGAA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG	60
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG	120
GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAC AGCCCTGCCA CACTTGGCCA	180
CCTCCCTTT GGGACCAGCA ATGT	204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA	60
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAA AGTTAGAAAT GTATAAAACA	120
CCATCAGACA GGTTTTAAA AAACAAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA	180
AAAACTTCTT GTATCAATT CTTTGTTC AATGACTGA CTTAANTATT TTTAAATATT	240
TCAAAACAC TTCTCTAAA ATTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCC	300
ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCAACC CACCACAAGC TTTCTGGGC	360
ATGCAACAGT GTCTTTCTT TNCTTTTCTT TTTTTTTTT TTACAGGCAC AGAAACTCAT	420

CAATTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT ATCACTCTTG T	480 491
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(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTAA GCAGGGCTAA TTACCATAAG ATGCTATTAA TTAANAGGTN TATGATCTGA GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTG CTTTGATAAC ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAC ATTAGCTGCT CAATCAAATC TCTACATAAC ACTATAGTAA TTAAAACGTT AAAAAAAAGT GTTGAAATCT GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC AGCTTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTG GCCTCTCCCT AATGATTGGC AGGTCTNGGT AATNCCAAAA CATATTCAA CTCAACACTT CTTTTCCNCG TANCTTGANT CTGTGTATTG CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTT CANT	60 120 180 240 300 360 420 480 484
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(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG TCTATGTCCT CTCAAGTGCC TTTTTGTTTG T	60 120 151
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(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCCACGG TCCCCAGAAC GGACACTTC	60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTG GSTATCTGTGG GTTGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAC TGT	133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GCAGGGT	147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGAAAATAC ATTGAATTTT CTGTATACTC	60
TGATTACATA CATTATCCT TTAAAAAAGA TCTAAATCTT AATTTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACGTGAATT TTAACTAGTT	180
TTGACTTCTA AGTTTGTT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAAGTTA TCAAAAACTC ACTCAATTTT	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT	60
GGTTGTTGCT CTTCAACAGT ATCCTCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA	30
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(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCCT TTGCTCTTCA AAACTGACCA TCTTTATAT TTAATGCTTC	60
CTGTATGAAT AAAAATGGTT ATGTCAAGT	89

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG	60
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT	97

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAACCT GGAACCCCCT TTTGATGGCA	60
GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC	120
CCAACCCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT	180
TCGGTCATAA NATGAAATCC CAANGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA	240
GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG	300
TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG	360
GGCGGGGAGG AGCATGT	377

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG	60
------------------------------------------------------------------	----

AGAACCCGTG TGCCCCTTCC CACCATATCC ACCCTCGCTC CATCTTGAA CTCAAACACG	120
AGGAACTAAC TGCACCCCTGG TCCTCTCCCC AGTCCCCAGT TCACCCCTCCA TCCCTCACCT	180
TCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT	240
TTATATATTT TTTAATAAGA TGCACTTTAT GTCATTTTT AATAAAGTCT GAAGAATTAC	300
TGTTT	305

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTTGTCC CAGCACTTAA GGAATGCTGA	60
GGTCGGACCA GCCACATCTC ATGTGCAAGA TTGCCCAGCA GACATCAGGT CTGAGAGTTC	120
CCCTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC	180
TGTGCTGTCC TGGAGATTCA CTTTGAGAG AGTTCTCCTC TGAGACCTGA TCTTAGAGG	240
CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG	300
CCTCTCCAG GGCCCCAGCC TGGCCACACC TGCTTACAGG GCACCTCTAG ATGCCCATAC	360
CATAGTTCT GTGCTAGTGG ACCGT	385

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTTTTTAA TGG	73

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGGCTC	TCACCCCTCCT	CTCCTGCAGC	60
TCCAGCTTG	TGCTCTGCC	CTGAGGAGAC	CATGGCCCAG	CATCTGAGTA	CCCTGCTGCT	120
CCTGCTGGCC	ACCCTAGCTG	TGGCCCTGGC	CTGGAGCCCC	AAGGAGGAGG	ATAGGATAAT	180
CCCGGGTGGC	ATCTATAACG	CAGACCTCAA	TGATGAGTGG	GTACAGCGTG	CCCTTCAC	240
CGCCATCAGC	GAGTATAACA	AGGCCACAA	AGATGACTAC	TACAGACGTC	CGCTGCGGGT	300
ACTAAGAGCC	AGGCAACAGA	CCGTTGGGG	GGTGAATTAC	TTCTTCGACG	TAGAGGTGGG	360
CCGAACCATA	TGTACCAAGT	CCCAGCCAA	CTTGGACACC	TGTGCCTTCC	ATGAACAGCC	420
AGAACTGCAG	AAGAAACAGT	TGTGCTCTT	CGAGATCTAC	GAAGTTCCCT	GGGGAGAAC	480
GAANGTCCCT	GGGTGAAATC	CAGGTGTCAA	GAAATCCTAN	GGATCTGTTG	CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA	ACAGGGGCC	TCTCAGCCCT	CCTAATGACC	TCCGGCTAG	CCATGTGATT	60
TCACTTCCAC	TCCATAACCGC	TCCTCATACT	AGGCCTACTA	ACCAACACAC	TAACCATATA	120
CCAATGATGG	CGCGATGTA	CACGAGAAAG	CACATACCA	GGCCACCACA	CACCACTG	180
CCAAAAAGGC	CTTCGATACG	GGATAATCCT	ATTATTACC	TCAGAAGTTT	TTTTCTTCGC	240
AGGGATTTT	CTGAGCCTT	TACCACTCCA	GCCTAGCCC	TACCCCCAA	CTAGGAGGGC	300
ACTGGCCCC	AACAGGCATC	ACCCCGCTAA	ATCCCCTAGA	AGTCCCAC	CTAAACACAT	360
CCGTATTACT	CGCATCAGGA	GTATCAATCA	CCTGAGCTCA	CCATAGTCTA	ATAGAAAACA	420
ACCGAAACCA	AATTATTCAA	AGCACTGCTT	ATTACAATT	TACTGGGTCT	CTATTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCACACACA	TTTCTACAT AGATAGTACT	60
AGGTATTAAT AGATATGTAA AGAAAAGAAAT CACACCATT	ATAATGGTAA GATTGGTTA	120
TGTGATTTA GTGGTATTT TGGCACCCCT ATATATGTTT	TCCAAACTT CAGCACTGAT	180
ATTATTTCCA TAACCTAAAA AGTGAGTTTG AAAAGAAAAA	TCTCCAGCAA GCATCTCATT	240
TAAATAAAGG TTGTCATCT TAAAGAACAC AGCAATATGT	GACTTTTAA AAAAGCTGTC	300
AAATAGGTGT GACCCACTA ATAATTATTA GAAATACATT	TAACACATC GAGTACCTCA	360
AGTCAGTTG CCTTGAAAAA TATCAAATAT AACTCTTAGA	GAAATGTACA TAAAAGAATG	420
CTTGTAAATT TTGGAGTANG AGGTTCCCTC CTCATTGTTG	TATTTTAAA AAGTACATGG	480
AAAAAAAAAA AATTACACAA AC AGTATATAAG GCTGTAAAAT	GAAGAATTCT GCC	533

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 511 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA ANACTGCTTC AGGGCGTGTA	60
AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC TAAAAGAGGG ACAAGGCTAA	120
AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTTGGG TTGGCTGGAG GAGCTGTGGA	180
AAACATGGAN AGATTGGTGC TGGANATCGC CGTGGCTATT CCTCATTGTT ATTACANAGT	240
GAGGTTCTCT GTGTGCCAC TGGTTTGAAA ACCGTTCTNC AATAATGATA GAATAGTACA	300
CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC CAACTAGATC CTCAGAANAC	360
GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC TTGTGCCCTT GTCTGTTATG	420
ATTTCTCTCC ATTGCAGCNA NAAACCGTT CTTCTAAGCA AACNCAGGTG ATGATGGCNA	480
AAATACACCC CCTCTTGAAAG NACCNGGAGG A	511

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC ACTGGTGCCA GTACCAGTAC CAATAACAGT GCCAGTGCCA GTGCCAGCAC	60
CAGTGGTGGC TTCAGTGTG TGCCAGCCT GACCGCCACT CTCACATTTG GGCTCTTCGC	120
TGGCCTTGGT GGAGCTGGTG CCAGCACCG AGTGGCAGCTCT GGTGCCTGTG GTTTCTCCTA	180
CAAGTGAGAT TTTAGATATT GTTAATCCTG CCAGTCTTC TCTTCAAGCC AGGGTGCATC	240

CTCAGAAACC TACTAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA	300
CTCTGCATTA AATCTATTTG CCATTTCTGA AAAAAAAA AAAAAAAGGG CGGCCGCTCG	360
ANTCTAGAGG GCCCGTTAA ACCCGTGTAT CAGCCTCGAC TGTGCCTCT ANTTGCCAGC	420
CATCTGTTGT TTGCCCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCCACT	480
GTCCTTCCT AANTAAAAT	499

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATT GGATTCAAGCC GCGAAGAGAT	60
TTATCAGCTT AACTCAGATA AAATCAATTGA AAGTAATAAG GTAAAAGCTA GTCTCTAACT	120
TCCAGGCCCA CGGCTCAAGT GAATTGAAAT ACTGCATTAA CAGTGTAGAG TAACACATAA	180
CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTACCACT CTAATCAAGA	240
AAAGAATTAC AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAAAATGG TAATCATTAG	300
GGCTTTGAT TTATAANACT TTGGGTACTT ATACTAAATT ATGGTAGTTA TACTGCCCTC	360
CAGTTTGCTT GATATATTG TTGATATTAA GATTCTTGAC TTATATTG AATGGGTTCT	420
ACTGAAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTATTTA CACTCTTGAT	480
TCTACAATGT AGAAAATGAA GGAAATGCC CAAATTGTAT GGTGATAAAA GTCCCGT	537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT TGTTCAAAAG ATGCAAATGA TACACTACTG CTGCAGCTCA CAAACACCTC	60
TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTTT GCCATCATCA	120
CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA TAACAGACGG	180
TGGCACAAAGG AGGCCATCTT TTCCTCATCG GTTATTGTCC CTAGAACCGT CTTCTGAGGA	240
TCTAGTTGGG CTTTCTTTCT GGGTTGGGC CATTTCANTT CTCATGTGTG TACTATTCTA	300
TCATTATTGT ATAACGGTTT TCAAACCNGT GGGCACNCAG AGAACCTCAC TCTGTAATAA	360
CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTNT TCCAGAGCTC	420
CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACAA TCCCTGN	467

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTCGGGCC	GAGATGTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCGCGCTAC	60
TCTCTCTTTC	TGGCCTGGAG	GCTATCCAGC	GTACTCCAAA	GATTCAAGTT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTTC	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180
CCGACATTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAGAAT	TGAAAAAGTG	GAGCATTGAG	240
ACTTGCTTT	CAGCAAGGAC	TGGTCTTCT	ATCTCTTGTA	CTACACTGAA	TTCACCCCCA	300
CTGAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTACAG	CCCAAGATNG	360
TTNAGTGGGA	TCGANACATG	TAAGCAGCAN	CATGGGAGGT			400

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC	TTGGTGTTC	AAGCCCTGC	AGGAAGCAGA	ATGCACCTTC	TGAGGCACCT	60
CCAGCTGCC	CGGCGGGGG	TGCGAGGCTC	GGAGCACCC	TGCCC GGCTG	TGATTGCTGC	120
CAGGCACTGT	TCATCTCAGC	TTTTCTGTCC	CTTTGCTCCC	GGCAAGCGCT	TCTGCTGAAA	180
GTTCATATCT	GGAGCCTGAT	GTCTAACGA	ATAAAGGTCC	CATGCTCCAC	CCGAAAAAAA	240
AAAAAAAAA						248

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTAACA	60
TCACCCAGAC CCCGCCCTGC CGCGCCCAA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTT ATAATGCCT	180
GATTAAAAAA AAAAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTGTT AGGTTTTGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG	60
TTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCGTGTT TTACTTTCT ATTCTTTATT	120
CCTCTTCTT CTGAAGATTG ATGAAGTTGA AAATTGAGGT GGATAAAATAC AAAAAGGTAG	180
TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT	300
CTGTCCTTG GCTAGAAAAA ATTATAAACAA GGACTTTGTT AGTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAA GTGGGCTAT ACATAAANTAA TNAAGAAATA TCCAATTAA	420
TTCCCAGGAA TATGGGGTTC ATTTATGAAAT ANTACCCGGG ANAGAAGTT TGANTNAAAC	480
CNGTTTGTT TAATACGTTA ATATGCTCTN AATNAACAAG GCNTGACTTA TTTCAAAAAA	540
AAAAAAA AA	552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTG GAGATGCTAA GGCCCCAGAG ATCGTTGAT CCAACCCCTCT TATTTTCAGA	60
GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TGCGCTGGCA CCCCTGGCCT	120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCAACACAGT CACTGAAGCA GGCCCTGTTT	180
GCAATTCACTG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA	240
AGGTTAAACT TTCCCACCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC	300

TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC	360
TCTTGGCTTT CTCATAAAA TCTCTATCCA TCTCATGTTT AATTTGGTAC GCNTAAAAAT	420
GCTGAAAAAA TTAAAATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAA AAAAAAA	476

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCCTGGA GGAGCCCAGT	60
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCCCTCCA TTCCCAGCCT	120
CTCATCCCCA TCTTGCACCTT TTGCTAGGGT TGGAGGCGCT TTCCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGGAAATAAG TCCTAGGGT GGGGGGTGTG GCAAGCCGGC CT	232

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCAGGGAGC AGAACGCTAAA GCCAAAGCCC AAGAACAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAT GCCAGTGCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACCGCCACT CTCACATTG GGCTCTTCGC TGGCCTGGT GGAGCTGGTG	180
CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTTCCTCCTA CAAGTGAGAT TTTAGATATT	240
GTAAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTTG	360
CCATTTCAAA AAAAAAAA AAA	383

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TC GGACTGTG	300
AGCCCTGATG CCTTTTGCC AGCCATACTC TTGGCNTCC AGTCTCTCGT GGCGATTGAT	360
TATGTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTT	420
TTTCNCATAT TTTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAAAA AAAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGCA GATTCCCCAG	120
GAGGACATGG AC GTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCTC CTGGGGCCCA GGCGGCACC TCGTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCAAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTCAAG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC CTCCACAAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC	60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA	120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG	180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCCAC ACTTTGATG ACTTTATTGA	240
GTGGATTCTG CATGTCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAGCC	300
CTATCATGCC NTTGAACGTG CCGAAGAACCA CCGAGCCTTG TGTGGGGGT GNAGTCTCAC	360
CCAGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACCTCGC CCAGGNNGAA	420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCCNT TGGTGGNNNGC GCNTNCCTTT	480
T	481

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGCTG AGAATTCAATT	60
ACTTGGAAAA GCAACTTNAA GCCTGGACAC TGGTATTAAA ATTCAACAATA TGCAACACTT	120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTCAATCACC AGTCTGGAA TAAGGGTATG	180
CCCTATTCAAC ACCTGTTAAA AGGGGCTAA GCATTTTGAT TTCAACATCT TTTTTTTGAT	240
CACAAGTCAG AAAAAGCAA AAGTAAACAG TTNTTAATTT GTTAGCCAAT TCACCTTCCTT	300
CATGGGACAG AGCCATTGAT TTTAAAAGC AAATTGCAATAATTTGAGCT TTGGGAGCTG	360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAAGACA CAACTCCCTT CATATTGGGA	420
TGTTNACNAA AGTTATGTCT CTTACAGATG GGATGCTTTT GTGGCAATTC TG	472

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCAGT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG	60
TGTGTGTGCG CGCATATTAT ATAGACAGGG ACATCTTTTT TACTTTGTAAAGCTTATG	120
CCTCTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TTGTCTTCTG TGTAAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT	240
TTTATTGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG	300
GGGGACAAAG AAAAGCANAACCTGAC GAAACAATTN CCTGGTGAGA AATTNCATAA	360

ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTT TTT

413

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCAC TCCC CGCGTCCCGC	60
GTCCTAGCCN ACCATGGCCG GGCCCCCTGCG CGCCCCGCTG CTCCCTGCTGG CCATCCTGGC	120
CGTGGCCCTG GCCGTGAGCC CGCGGCCCG CGTCCAGTCCC GGCAAGCCGC CGCGCCTGGT	180
GGGAGGCCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCGTGCACTG GACTTTGCCG	240
TCGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC	300
CCCAANCAAA TTGTTACTNG GGGTAANTAA TTCTTGGAAAG TTGAACCTGG GCCAAACNNG	360
TTTACCAAGAA CCNAGCCAAT TNGAACAAATT NCCCCTCCAT AACAGCCCT TTTAAAAAGG	420
GAANCANTCC TGNTCTTTTC CAAATTTC	448

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTGTG CACTGGCAC TGTGATGGAA CCATTGGCC AGGATGCTTT GAGTTTATCA	60
GTAGTGATT TGCCAAAGTT GGTGTTGAA CATGAGTATG TAAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTTGATG CCTTGAAGTT	180
CTCAGTGACA AGTTNNNTCT GATGCGAAGT TCTNATTCCA GTGTTTAGT CCTTTGCATC	240
TTTNATGTTN AGACTTGCT CTNTNAAATT GCTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTTAACAAAA TAGAANNACT TCTCTGTTN GAANATTITGA ATATCTTACA TCTNAAAATN	360
AATTCTCTCC CCATANNAAA ACCCANGCCC TTGGGANAAT TTGAAAAANG GNTCCTTCNN	420
AATTCNNANA ANTTCAGNTN TCATACAAACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA GGTCTNTTNT ACTGTCGGAC TGTTCANCCA CCAACTCTAC AAGTTGCTGT	60
CTTCCACTCA CTGTCGTAA GCNTNTAAC CCAGACTGTA TCTTCATAAA TAGAACAAAT	120
TCTTCACCAG TCACATCTTC TAGGACCTTT TTGGATTCAAG TTAGTATAAG CTCTTCCACT	180
TCCTTGTAA AGACTTCATC TGGTAAAGTC TTAAGTTTG TAGAAAGGAA TTTAATTGCT	240
CGTTCTCTAA CAATGTCCTC TCCTTGAAGT ATTTGGCTGA ACAACCCACC TNAAGTCCCT	300
TTGTGCATCC ATTTTAAATA TACTTAATAG GGCATTGGTN CACTAGGTTA AATTCTGCCA	360
GAGTCATCTG TCTGCAAAAG TTGCGTTAGT ATATCTGCCA	400

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT	60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCAATTCCC TGAGTCAGAC	120
ATGCCTCTTT GACTACCGTG TGCCAGTGCT GGTGATTCTC ACACACCTCC NNCCGCTCTT	180
TGTGGAAAAA CTGGCACTTG NCTGGAACATA GCAAGACATC ACTTACAAAT TCACCCACGA	240
GACACTTGAA AGGTGTAACA AAGCGACTCT TGCAATTGCTT TTTGTCCCTC CGGCACCAGT	300
TGTCAAATACT AACCCGCTGG TTTGCCTCCA TCACATTGT GATCTGTAGC TCTGGATACA	360
TCTCCTGACA GTACTGAAGA ACTTCTTCTT TTGTTTCAAAGCAACTCTT GGTGCCTGTT	420
NGATCAGGTT CCCATTTCCC AGTCCGAATG TTCACATGGC ATATNTTACT TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCCCA NATCCCACCA CGAACAGATGCG CTTGTTGACT GAGAACCTGA TGCGGTCACT	60
GGTCCCGCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGGTTGATGC TGCACTCCTT	120
CCCACCGCAGG CAGCAGCGGG GCCGGTCAAT GAACCTCACT CGTGGCTTGG GGTTGACGGT	180
TAANTGCAGG AAGAGGCTGA CCACCTCGCG GTCCACCAGG ATGCCCGACT GTGCGGGACC	240
TGCAGCGAAA CCTCTCGATG GTCATGAGCG GGAAGCGAAT GANGCCCAGG GCCTTGCCCCA	300
GAACCTTCCG CCTGTTCTCT GGCGTCAACCT GCAGCTGCTG CCGCTNACAC TCGGCCCTCGG	360
ACCAGCGGAC AAACAGGGCTT GAACAGCCGC ACCTCACGGA TGCCCANTGT GTCGCGCTCC	420
AGGAACGGCN CCAGCGTGTGTC CAGGTCAATG TCGGTGAANC CTCCGCGGGT AATGGCG	477

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG ACCTTGCTC GCATTGTGCT GCTGGCAGGA ATACCTTGGC AAGCAGCTCC	60
AGTCCGAGCA GCCCCAGACC GCTGCCGCC GAAGCTAACGC CTGCCTCTGG CCTTCCCCCTC	120
CGCCTCAATG CAGAACCCANT AGTGGGAGCA CTGTGTTTAG AGTTAAGAGT GAACACTGTN	180
TGATTTTACT TGGGAATTTC CTCTGTTATA TAGCTTTTCC CAATGCTAAT TTCCAAACAA	240
CAACAAACAAA ATAACATGTT TGCCTGTTNA GTTGTATAAA AGTANGTGAT TCTGTATNTA	300
AAGAAAATAT TACTGTTACA TATACTGCTT GCAANTTCTG TATTTATTGG TNCTCTGGAA	360
ATAAAATATAT TATTAAA	377

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG GGTTAGGGTC CAGTTCCCAG TGGAAGAAC AGGCCAGGAG AANTGCGTGC	60
CGAGCTGANG CAGATTTCAC ACAGTGACCC CAGAGCCCTG GGCTATAGTC TCTGACCCCT	120
CCAAGGAAAG ACCACCTTCT GGGGACATGG GCTGGAGGGC AGGACCTAGA GGCACCAAGG	180
GAAGGCCCCA TTCCGGGGCT GTTCCCCGAG GAGGAAGGGGA AGGGGCTCTG TGTGCCCCCC	240
ACGAGGAANA GGCCCTGANT CCTGGGATCA NACACCCCTT CACGTGTATC CCCACACAAA	300

TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCACTGGCCC	360
ACACCCACCC AGANCANCCA CCCGCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG	420
TGGACTCTNG TCCCNNAAAGG GGGCAGAATC TCCAATAGAN GGANNGAAC CTTGCTNANA	480
AAAAAAAANA AAAAAA	495

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG TTTCATGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGCTGCTC	60
CCTCTGGAAG CCTTGCAG AGCGGACTTT GTAATTGTT GAGAATAACT GCTGAATTT	120
TAGCTGTTT GAGTTGATTC GCACCACTGC ACCACAACTC AATATGAAAA CTATTTNACT	180
TATTTATTAT CTTGTGAAAA GTATACAATG AAAATTTGT TCATACTGTA TTTATCAAGT	240
ATGATGAAAA GCAATAGATA TATATTCTTT TATTATGTTN AATTATGATT GCCATTATTA	300
ATCGGCAAAA TGTTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCTTTT GTAACCTCAC	360
TTGGTTATT TATTGTAAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA	420
TTTANTTCAN TAATTCTTT CCTTGTAC GTTAATTG AAAAGAATGC AT	472

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAT	60
GTGGTGAAT TTCAAAATTA TATGTAACCT CTACTAGTTT TACTTTCTCC CCCAAGTCTT	120
TTTTAACTCA TGATTTTAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT	180
ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAGTGTCTT GNGCANAATG TTCTAGNTAT	240
AGCTGGATAC ATACNGTGGG AGTTCTATAA ACTCATACCT CAGTGGGACT NAACCCAAAT	300
TGTGTTAGTC TCAATTCTTA CCACACTGAG GGAGCCTCCC AAATCACTAT ATTCTTATCT	360
GCAGGTACTC CTCCAGAAAA ACNGACAGGG CAGGCTTGCA TGAAAAGTN ACATCTGCGT	420
TACAAAGTCT ATCTTCCTCA NANGTCTGTN AAGGAACAAT TTAATCTTCT AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA	ATGCTGATAT	GATCTTGAGT	ATAAGAACAT	ATATGTCAC	AGAACGGATA	60
AAATAATGCT	GCAAACTTAA	TGTTCTTATG	CAAATGGAA	CGCTAATGAA	ACACAGCTTA	120
CAATCGAAA	TCAAAACTCA	CAAGTGCCTCA	TCTGTTGTAG	ATTTAGTGTAA	ATAAGACTTA	180
GATTGTGCTC	CTTCGGATAT	GATTGTTTCT	CANATCTGG	GCAATNTTCC	TTAGTCAAAT	240
CAGGCTACTA	GAATTCTGTT	ATTGGATATN	TGAGAGCATG	AAATTTTAA	NAATACACTT	300
GTGATTATNA	AATTAATCAC	AAATTTCACT	TATACCTGCT	ATCAGCAGCT	AGAAAAACAT	360
NTNNNTTTTA	NATCAAAGTA	TTTTGTTTTT	CCAANTGTNN	AAATGAAATC	TGAATGTGGG	420
TTCNATCTTA	TTTTTCCCN	GACNACTANT	TNCTTTTTTA	GGGNCTATTTC	TGANCCATC	479

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTTCAG	TTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCACT	CTGAACACGCC	TGGTTATCTA	GATGAGAACA	GAGAAATAAA	GTCAGAAAAT	300
TTACCTGGAG	AAAAGAGGCT	TTGGCTGGGG	ACCATCCCCT	TGAACCTTCT	CTTAAGGACT	360
TTAAGAAAAAA	CTACCACATG	TTGTGTATCC	TGGTGCCGGC	CGTTTATGAA	CTGACCACCC	420
TTTCCAATAA	TCTTGACGCT	CCTGAACCTTG	CTCCCTCTGCG	A		461

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC	GCAGGGTGT	TTT CCTCGTACCG	CAGGGCCCCC	TCCCTCCCC	AGGC GTCCCT	60
CGGCGCCTCT	GC GGGCCCGA	GGAGGAGCGG	CTGGCGGGTG	GGGGGAGTGT	GACCCACCC	120
CGGTGAGAAA	AGCCTTCTCT	AGCGATCTGA	GAGGCGTGCC	TTGGGGGTAC C		171

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG	TGCAACTCCA	GCTGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGCG	GCGACAGTCG	CAGGTGCAGC	GCGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAAGCGGGAG	'GCCTCGGGGA	GCCCCTCGGG	AAGGGCGGCC	240
CGAGAGATAAC	GCAGGTGCAG	GTGGCCGCC				269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTT	TTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTCTGTGG	120
TTGATTGGTT	TGTCTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAACGAAGCA	AATAACATGG	180
AGTGGGTGCA	CCCTCCCTGT	AGAACCTGGT	TACAAAGCTT	GGGGCAGTTC	ACCTGGTCTG	240
TGACCGTCAT	TTTCTTGACA	TCAATGTTAT	TAGAAGTCAG	GATATCTTTT	AGAGAGTCCA	300
CTGTTCTGGA	GGGAGATTAG	GGTTTCTTGC	CAAATCCAAC	AAAATCCACT	AAAAAAGTTG	360
GATGATCAGT	ACGAATAACCG	AGGCATATTC	TCATATCGGT	GGCCA		405

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	60
GGCACTTAAT CCATTTTTAT TTCAAAATGT CTACAAATT T AATCCCATTA TACGGTATTT	120
TCAAAATCTA ATTATTCAA ATTAGCCAA TCCTTACCAA ATAATACCCA AAAATCAAAA	180
ATATACTTCT TTCAGCAAAC TTGTTACATA AATTAAAAAA ATATATACGG CTGGTGTTTT	240
CAAAGTACAA TTATCTAAC ACTGCAAACA TTTTAAGGAA CTAAAATAAA AAAAAACACT	300
CCGCAAAGGT TAAAGGGAAC AACAAATTCT TTTACAACAC CATTATAAAA ATCATATCTC	360
AAATCTTAGG GGAATATATA CTTCACACGG GATCTTAACT TTTACTCACT TTGTTTATTT	420
TTTTAAACCA TTGTTGGGC CCAACACAAT GGAATCCCCC CTGGACTAGT	470

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 581 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTT TTTTTTTG A CCCCCCTCTT ATAAAAAAC A AGTTACCATT TTATTTACT	60
TACACATATT TATTTCATAA TTGGTATTAG ATATTCAAAA GGCAGCTTT AAAATCAAAC	120
TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATT A GCTTAAAATC TGCTAAAGT	180
GAAAATCTC TCTAGCTCTT TTGACTGTAA ATTTTGACT CTTGTAAAAC ATCCAAATTC	240
ATTTTTCTTG TCTTTAAAAT TATCTAATCT TCCCATTTT TCCCTATTCC AAGTCAATT	300
GCTTCTCTAG CCTCATTCC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTCTAAA	360
AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTCA T ATTCTACCT	420
ACGTTAATAA AATAGCATT TGTGAAGCCA GCTCAAAAGA AGGCTTAGAT CCTTTATGT	480
CCATTTAGT CACTAACAGA TATCAAAGTG CCAGAATGCA AAAGGTTGT GAACATTAT	540
TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTCT G	581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 578 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT TTTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGACTTTT	60
CACTCTCTAG ATAGGGCATG AAGAAAACTC ATCTTCCAG CTTTAAAATA ACAATCAAAT	120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTTCTCCTGA	180
AGGAAATCTG TTCATTCTTC TCATTCAAT AGTTATATCA AGTACTACCT TGCAATTG	240
GAGGTTCCTC TTCTCTATT ACACATATAT TTCCATGTGA ATTGTATCA AACCTTATT	300
TTCATGCAA CTAGAAAATA ATGTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATTA	360
CAAAACTGCT CAAATTGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC	420
AAATCACATT TACGACAGCA ATAATAAAAC TGAAGTACCA GTTAAATATC CAAAATAATT	480
AAAGGAACAT TTTTAGCCCG GGTATAATTA GCTAATTACAC TTTACAAGCA TTTATTAGAA	540
TGAATTACACA TGTTATTATT CCTAGCCCAA CACAATGG	578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTTT TTTTCAGTA ATAATCAGAA CAATATTTAT TTTTATATTT AAAATTCTATA	60
GAAAGTGCC TTACATTAA TAAAAGTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT	120
GTCTTGAACA CCAATATTAA TTTGAGGAAA ATACACCAAA ATACATTAAG TAAATTATTT	180
AAGATCATAG AGCTTGTAG TGAAAAGATA AAATTTGACC TCAGAAACTC TGAGCATTAA	240
AAATCCACTA TTAGCAAATA AATTACTATG GACTTCTTGC TTTAATTGG TGATGAATAT	300
GGGGTGTAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA	360
TGTACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTCT CTTCTTCAA TCTTTAAGG	420
GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCATACT GTTCTTCTA TGGAAGGATT	480
AGATATGTTT CCTTGCCCAA TATTAATGTT TACTACTAG TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT TTTTTTAGTC AAGTTTCTAT TTTTATTATA ATTAAAGTCT TGGTCATTTC	60
ATTTATTAGC TCTGCAACTT ACATATTAA ATTAAAGAAA CGTTTTAGAC AACTGTACAA	120
TTTATAAAATG TAAGGTGCCA TTATTGAGTA ATATATTCCCT CCAAGAGTGG ATGTGTCCCT	180
TCTCCCACCA ACTAATGAAC AGCAACATTA GTTTAATTTC ATTAGTAGAT ATACACTGCT	240
GCAAACGCTA ATTCTCTCT CCATCCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG	300
AATGCATCAC AATCTACAAT CAACAGCAAG ATGAAGCTAG GCTGGGCTTT CGGTGAAAAT	360
AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCCTC GGTGGCAAGA ACTCTTCGAA	420
CCGCTTCCCTC AAAGGCGCTG CCACATTGT GGCTCTTGC ACTTGTTCGA AAA	473

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA CTGCAGGGCA TCTCGGTCAT GGAGCTGTCC GGCCTGGCCC CGGGCCCGTT	60
CTGTGCTATG GTCCTGGCTG ACTTCGGGGC CGGTGTGGTA CGCGTGGACC GGCCCGGCTC	120
CCGCTACGAC GTGAGCCGCT TGGGCGGGGG CAAGCGCTCG CTAGTGTCTG ACCTGAAGCA	180
GCCGCGGGGA GCCGCGGTGC TGCGGGGTCT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC	240
CTTCCGCCGC GGTGTCATGG AGAAACTCCA GCTGGGCCA GAGATTCTGC AGCGGGAAAA	300
TCCAAGGCTT ATTTATGCCA GGCTGAGTGG ATTGGCCAG TCAGGAAGCT TCTGCCGGTT	360
AGCTGGCCAC GATATCAACT ATTTGGCTTT GTCAGGTGTT CTCTCAAAAA TTGGCAGAAC	420
TGGTGAGAAT CCGTATGCCA CGCTGAATCT CCTGGCTGAC TTTGCTGGTG GTGGCCTTAT	480
GTGTGCACTG GGCATTATAA TGGCTTTTG TGACCGACA CGCACTGACA AGGGTCAGGT	540
CATTGATGCA AATATGGTG AAGGAACAGC ATATTTAAGT TCTTTCTGT GGAAAACCTCA	600
GAAATCGAGT CTGTTGGAAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTT	660
CTATACGACT TACAGGACAG CAGATGGGG ATTCACTGGCT GTTGGAGCAA TAGAACCCCA	720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTTC CCAATCAGAT	780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTGCA GATGTATTTG CAAAGAACAG	840
GAAGGCAGAG TGGTGTCAA TCTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC	900
TTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTA TCACCAGTGA	960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTT AACACCCAG CCATCCCTTC	1020
TTTCAAAAGG GATCCTTCA TAGGAGAACAA CACTGAGGAG ATACTTGAAG AATTTGGATT	1080
CAGCCGCGAA GAGATTTCATC AGCTTAACCTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA	1140
AGCTAGTCTC TAACTTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG	1200
TAGAGTAACA CATAACATG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCTA	1260
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGTGATT GAATTCTAAA	1320
AATGGTTATC ATTAGGGCTT TTGATTATA AAACATTGGG TACTTATACT AAATTATGGT	1380
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATT TTGACTTATA	1440
TTTGAAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATT	1500
ATTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT	1560

AAAAAGTCACG TGAAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1620
A	1621

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
 1           5           10          15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
 20          25          30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
 35          40          45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
 50          55          60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
 65          70          75          80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
 85          90          95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
 100         105         110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
 115         120         125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
 130         135         140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys
 145         150         155         160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
 165         170         175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
 180         185         190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
 195         200         205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
 210         215         220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
 225         230         235         240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
 245         250         255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260         265         270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275         280         285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val

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290	295	300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu		
305	310	315
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala		
	325	330
Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu		
	340	345
Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn		
	355	360
Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu		
	370	375
		380

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCTCACT	GAGCCAGCGC	CTGCGCCTCT	ACCTCGCCGA	CAGCTGGAAC	120
CAGTGCACC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGTACC	ACCTGGCCG	CACTGTCCTC	TGCATCGACT	TCATGGTTTT	CACGGTGCGG	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCCTTTC	TTCTCGGCG	TGTGGCTGGT	AGCTTATGGC	360
GTGCCACGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGA	TCCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGCAGATT	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCCAGGCGG	GCACCTGCGT	CTCCCACTAT	GCCAACCTGGC	TGGTGGTGCT	GCTCCCTCGTC	600
ATCTTCTGC	TCGTGGCCAA	CATCTGCTG	GTCAACTTGC	TCATTGCCAT	GTTCAGTTAC	660
ACATTCGGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTGGA	AGGCGCAGCG	TTACCGCCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCCGCGTG	GCCCCGCCCT	TTATCGTCAT	CTCCCACTTG	780
CGCCCTCTGC	TCAGGCAATT	GTGCAGGCGA	CCCCGGAGCC	CCCAGCCGTC	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTCTAAG	GAAGCCGAGC	GGAAAGCTGCT	AACGTGGAA	900
TCGGTGCATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAAGGTG	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCCGTC	1080
CTGGGGTGGG	TGGCCGAGGC	CCTGAGCCGC	TCTGCCCTTG	TGCCCCCAGG	TGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAAGCCC	1200
CCACAGGGGA	TTTTGCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCCCCC	GCACCTGGTG	1260
GCCTTGTCCCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTGGGA	1320
GTGTCATCCT	TACAAACCCAC	AGCATGCCG	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380
GGATCAAGGC	CTGGATCCCG	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACCAC	AGACCCCTCA	CCACTCACAG	ATTCCCTACA	CTGGGGAAAT	AAAGCCATT	1500
CAGAGGAAAA	AAAAAAAAAA	AAAAA				1524

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCC	CACAGCAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATTC	CTAGGCAGTT	180
GGCAGCAGCA	AGGAGGAGAG	GCCGAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGGC	ACCGGAAAGC	CCAGCTTGTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCACTGT	CCTTGGGCAT	CCTGCTGAGC	CTCTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCGGA	TCCCAGGCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACTCCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTCGCCAG	GCCTACTCTG	TCTATGCCCTT	780
CATGATCAGT	CTTGGGGGCT	GCCTGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCAAG	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCCCAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTGCC	CACTGCTGTC	CATGCCGGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGGCGCCCT	GCTTCCCCTG	CTGCACCAGC	TGTGCTGCCG	1080
CATGCCCGC	ACCCCTGC	GGCTCTCGT	GGCTGAGCTG	TGCAGCTGG	TGGCACTCAT	1140
GACCTTCACG	CTGTTTTACA	CGGATTCG	GGGCGAGGGG	CTGTACCAGG	CGTGTCCCAG	1200
AGCTGAGCCG	GGCACCGAGG	CCCGGAGACA	CTATGATGAA	GGCGTTCGGA	TGGGAGCCT	1260
GGGGCTGTT	CTGCAGTGCG	CCATCTCCCT	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATTC	GGCACTCGAG	CAGTCTATT	GGCCAGTGTG	GCAGCTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCCTGTCCC	ACAGTGTGGC	CGTGGTACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTCACCTTC	TCAGCCCTGC	AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	1500
GAAGCAGGTG	TTCCTGCCCA	AATACCGAGG	GGACACTGGA	GGTGTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCCCTGC	CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCCACC	TCCACCCCGC	CTCTGCGGGG	CCTCTGCC	1680
TGATGTCTCC	GTACGTGTTG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCCTGGA	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATCCCTGTTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCACTGCC	ATATGGTGT	1860
TGCCGCAGGC	CTGGGTCTGG	TCGCCATTAA	CTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGG	GGGCGCTGCC	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCGCCTG	2160
ACTGGAGGCC	TTCCAAGGGG	GTTCAGTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACT	AGAGAAGGGT	TTTGGGAGC	TGAATAAACT	CAGTCACCTG	2340
GTTCCCATC	TCTAAGCCCC	TTAACCTGCA	GCTTCGTTA	ATGTAGCTCT	TGCATGGGAG	2400
TTTCTAGGAT	GAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTG	TAGGGGAAGA	2460

GTCCTGAGGG GCAACACACA AGAACCGAGT CCCCTCAGCC CACAGCACTG TCTTTTGCT	2520
GATCCACCCC CCTCTTACTT TTTATCAGGA TGTCGGCTGT TGGTCCTCT GTGCCATCA	2580
CAGAGACACA GGCATTTAAA TATTTAACTT ATTATTTAA CAAAGTAGAA GGGATCCAT	2640
TGCTAGCTTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA	2700
GGTCCCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTCTT CTCTGGGGT	2760
CTGGCCCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTCTACTCATCCC AAAATGATAAT	2820
TCCAAATGCT GTTACCCAAG GTTAGGGTGT TGAAGGAAGG TAGAGGTGG GGCTTCAGGT	2880
CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTTGGCCAG CCGGTTCCC CCCACTTCCA	2940
CTCCCCCTCTA CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAT TTCCCCTACC	3000
CCCAACTTTC CCCTACCCCC AACTTTCCCC ACCAGCTCCA CAACCCCTGTT TGGAGCTACT	3060
GCAGGACCAG AAGCACAAG TGCGGGTTCC CAAGCCTTTG TCCATCTCAG CCCCCAGAGT	3120
ATATCTGTGC TTGGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG	3180
GAGGTCTTAT CTCTCAGGGG GGGTTAACGT GCCGTTTGCA ATAATGTCGT CTTATTTATT	3240
TAGCGGGGTG AATATTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA	3300
AAATTAAGG CTTCTTATA TGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3360
AAAAAAAAA AAAAAAAAAA AAAAAAATAA AAAAAAAAAA	3410

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGGCGT CCCTCTGCCT GCCCACTCAG TGGCACACACC CGGGAGCTGT TTTGTCTTT	60
GTGGAGCCTC AGCAGTTCCC TCTTCAGAA CTCACTGCCA AGAGCCTGTA ACAGGAGCCA	120
CCATGCAGTG CTTCAGCTTC ATTAAGACCA TGATGATCCT CTTCAATTG CTCATCTTTC	180
TGTGTGGTGC AGCCCTGTTG GCAGTGGGCA TCTGGGTGTC AATCGATGGG GCATCCTTC	240
TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCAACGTG GGCTACTTCC	300
TCATCGCAGC CGGCCTTG TGCTTTGCTC TTGGTTTCCT GGGCTGCTAT GGTGCTAAGA	360
CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCTCATC TTCATTGCTG	420
AGGTTGCAGC TGCTGTGGTC GCCTTGGTGT ACACCACAAT GGCTGAGCAC TTCCTGACGT	480
TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCCA GGAAGACTTC ACTCAAGTGT	540
GGAACACACAC CATGAAAGGG CTCAAGTGCT GTGGCTTCAC CAACTATACG GATTTGAGG	600
ACTCACCCCTA CTTCAAAGAG AACAGTGCT TTCCCCCATT CTGTTGCAAT GACAACGTCA	660
CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGGCTCA CGACCAAAAA GTAGAGGGTT	720
GCTTCAATCA GCTTTGTAT GACATCCGAA CTAATGCAGT CACCGTGGGT GGTGTGGCAG	780
CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC	840
TACAATAAGT CCACTTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAACCT GTGAAGAGGG	900
ACCCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA	960
GAATGGACCT GCCCCTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CTTTTAGCG	1020
ATGCCTGACT TTCCCTCCAT TGTTGGGTGG ATGGGTGGGG GGCATTCAG AGCCTCTAAG	1080
GTAGCCAGTT CTGTTGCCA TTCCCCCAGT CTATTAACCT CTTGATATGC CCCCTAGGCC	1140
TAGTGGTGAT CCCAGTGCT TACTGGGGGA TGAGAGAAAG GCATTTATA GCCTGGGCAT	1200
AAGTGAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACC	1260
TGTTACAATG TTAAAAAAA AAAAAAAAAA	1289

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20 25 30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr

210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		
245	250	255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		
260	265	270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		
275	280	285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly		
290	295	300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		
305	310	315

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala		
1	5	10
		15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu		
20	25	30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Glu Val Gly Val		
35	40	45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly		
50	55	60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly		
65	70	75
		80

Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile		
85	90	95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu		
100	105	110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125

 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140

 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160

 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175

 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190

 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205

 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Ala Ala Leu Gly
 210 215 220

 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240

 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255

 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270

 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285

 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300

 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320

 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335

 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350

 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365

 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380

 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415

 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430

 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445

 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460

 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 480

 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495

 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510

 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525

 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540

 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1 5 10 15

 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30

 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45

 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

90

50	55	60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr		
65	70	75
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Ile		
85	90	95
Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr		
100	105	110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys		
115	120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met		
130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
160		
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		
165	170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		
180	185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		
195	200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		
210	215	220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu		
225	230	235
240		
Gln		

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: 'SEQ ID NO:115:

GCTCTTCTC	TCCCCTCCCT	TGAATTAAAT	TCTTCAACT	TGCAATTGC	AAGGATTACA	60
CATTCACTG	TGATGTATAT	TGTGTTGCAA	AAAAAAAAAA	GTGTCTTGT	TTAAAATTAC	120
TTGGTTGTG	AATCCATCTT	GCTTTTCCC	CATTGGAAC	AGTCATTAAC	CCATCTCTGA	180
ACTGGTAGAA	AAACATCTGA	AGAGCTAGTC	TATCAGCATC	TGACAGGTGA	ATTGGATGGT	240
TCTCAGAAC	ATTCACCCA	GACAGCCTGT	TTCTATCCTG	TTTAATAAAT	TAGTTGGGT	300
TCTCTACATG	CATAACAAAC	CCTGCTCCAA	TCTGTCACAT	AAAAGTCTGT	GACTTGAAAGT	360
						366
TTAGTC						

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA	ACCATTTCCT	ATATTATAGC	AAAATTAAAA	TCTACCGTA	TTCTAATATT	60
GAGAAATGAG	ATNAAACACA	ATNTTATAAA	GTCTACTTAG	AGAAGATCAA	GTGACCTCAA	120
AGACTTTACT	ATTTCATAT	TTTAAGACAC	ATGATTATC	CTATTTAGT	AACCTGGTTC	180
ATACGTTAAA	CAAAGGATAA	TGTGAACAGC	AGAGAGGATT	TGTTGGCAGA	AAATCTATGT	240
TCAATCTNGA	ACTATCTANA	TCACAGACAT	TTCTATTCC	TT		282

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG	CTTCACTGCC	TTCTTAGATG	CTTCTGGTCA	ACATANAGGA	ACAGGGACCA	60
TATTTATCCT	CCCTCCTGAA	ACAATTGCAA	ATAANACAA	AATATATGAA	ACAATTGCAA	120
AATAAGGCAA	AATATATGAA	ACAACAGGTC	TCGAGATATT	GGAAATCAGT	CAATGAAGGA	180
TACTGATCCC	TGATCACTGT	CCTAATGCAG	GATGTGGGAA	ACAGATGAGG	TCACCTCTGT	240
GAUTGCCCA	GCTTACTGCC	TGTAGAGAGT	TTCTANGCTG	CAGTTCAGAC	AGGGAGAAAT	300
						305
TGGGT						

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTG CCGCACAAATC TGAGTGGAAA	60
AANTCCTGGG T	71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA	60
GAAAATGGGG TGAAATTGGC CAACTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC	120
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT	180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT	212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC	60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT	90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANC GTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AAN CCTTGAA GTC ATTTTGA	60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATT CAT GGTTCTTTG GGAATTCC TT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCGGGGTCACT CTGTGCCACA GGTCCCTGTT GACAGTGC GG T	171

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA	50
TTATCAANTA TTGTGT	76

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCIITCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT	60
CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTT ATTCTCTTGG	120
TTAACAGATTG T	131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG	60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA	120
CTACAGTCCTG CATTGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT	180
TTGCCTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG	240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC	300
CATGGTGGGG GTCTTGATC TGTAAGAATG GAATTGATTT TGCTTTGCA AGAATCTCAG	360
CAGGAAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC	420
CTCTTGCTT GT	432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTG AATAGTAAAA TAGAAACTGA GCTGAAATT CTAATTCACT TTCTAACCAT	60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAAATT GT	112

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG	54
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(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGTCTCCCT CTACCGCTC	60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGC TCTCTGCTCA	120
TTCTCTCTGA AGTCTAGGTT ACCCATTTG GGGACCCATT ATAGGCAATA AACACAGTTC	180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTT TCTTAGCCTT	240
TTCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT	300
AGGCTGCCTT CTTTCCATG TCC	323

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATT TTAAATATCA CTTTGTATC ACTCTGACTT TITAGCATA	60
TGAAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCAA ATCATTCATC	120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAAC CTCTTGACA	60
TATAATGACG CAACAAAAAG GTGCTGTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTCCTATTG TGTTTGCGC ATCTTCTGGC TAATCGGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTG CATTGGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTATTTAAA AGCTTTATT TTGTGGTCAT TAAAATGGCA ATTTATGTGC AGCACTTTAT	300
TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTT GCTAATCTTA AAAAGTAATG	360
GG	362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGT TTAATGGAGT TTCCCAGTCA	60
GTANGACTGG TATGGTTGCA GCTGCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA	120
GTTCTCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTTTT AGGAGGCATC	180
TTCTGAAGTA GATTAAGGCA GCTTGAAAT CTGATGTGAT TTGGTTTATT ATCCAAGTAA	240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA TTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC	60
AGTGGCTAAC AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAC	120
CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTG TATCTCGGGT	180
TTTAGCAAGT TAAAATGAAN ATGACAGGAA AGGCTTATTG ATCAACAAAG AGAAGAGTTG	240
GGATGCTTCT AAAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT	300
GTAACAATCT ACAATTGGTC CA	322

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC ACAAGTTAA CTAAATTGGG ATTAATCTT CTGTANTTAT CTGCATAATT	60
CTTGTTTTTC TTTCCATCTG GCTCCTGGGT TGACAATTG TGGAAACAAC TCTATTGCTA	120
CTATTTAAAA AAAATCACAA ATCTTCCCT TTAAGCTATG TTNAATTCAA ACTATTCTG	180
CTATTCCTGT TTTGTCAAAG AAATTATATT TTCAAAATA TGTNTATTG TTTGATGGGT	240
CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG	278

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAA CTTGTTTAGC TCCATAGAGG AAAGAATGTT AAACTTGTA TTTTAAACA	60
TGATTCTCTG AGGTTAAACT TGGTTTCAA ATGTTATTT TACTTGTATT TTGCTTTGG	120
T	121

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC ATGCCTAGCA CATCAGAACAT CCTCAAAGAA CATCAGTATA ATCCTATACC	60
ATANCAAGTG GTGACTGGTT AAGCGTGCAG CAAAGGTCACTGGCACATT ACTTGTGTGC	120
AAACTTGATA CTTTTGTTCT AAGTAGGAAC TAGTATACAG TNCCCTAGGANTGGTACTCCA	180
GGGTGCCCGG CAAACTCCTGC AGCCGTCCT CTGTGCCAGNCCTGNAAGG AACTTTCGCT	240
CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAC GTTTGCTGAG	300
TTCCAAGGA TGCAAAGCCT GGTGCTCAAC TCCTGGGGCG TCAACTCAGT	350

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT	60
GCTGTGATTG TATCCGAATA NTCCCTGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT	120
GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA	180
CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCCT TTTGTGGTGA CAACNCCAAG	240
AAAACTGCAG AGGCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC	300
TCCCAGGAAC CGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG	360
GGTGCAGANG GATGAAGCAG CCAGNTGTTG TGCTGTGGT	399

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT	60
GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTTGGCC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGTT CCTGT	165

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC	60
TTAACTCTC CAGTAAGAAC CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCAA	120
TGCTGGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG	180
TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGA GGGCTGGGG CATANANGGT	240
CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTIGCCAC TGTACATTCC CCATNTTTAA	300
AAAAACTGAT GCCTTTTTT TTTTTTTTG TAAAATTC	338

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG GTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT AGTCCCCGAA GTGAAGGAGA	120
ATTCAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTGTG GCTCACCGCC TATCATCTGC	180

100

ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCCGTGAT GTCTGTAGTT TCACAGGATG	240
CCTTATTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT	300
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG	360
GCCTGGAAC TGTAAAGT GT	382

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAANCTT CTTTCTGTTG TGTTNGATT TACTATAGGG GTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG	120
TTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAT CACATATTTT	180
ATATTCAGCA TAAAGGAGAA	200

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAATAA AGTTGGTGG	60
GGGTGCTGAC TAAACCTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGTT	120
ATGCATGTAG AGAACCCAAA CTAATTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTTCTG AGAACCATCC AATTCACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTCTACC AGTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG	300
ATTCACAAAC CAAGTAATT TAAACAAAGA CACTT	335

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTTAA TATTGCCACA TATATCCTT CCAATTGCGG GCTAACAGA CGTGTATT	60
GGGTTGTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTT CATGGAGT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTGTTA TTCAGATAGC AGTCTGAT	180
CACATGGTCC ACAACACATC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAAACATC ATAGCCAATG ATGCCCCGCT TGCCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	360
AGCTACCACT AGCTACCACT TTGACTATNT TTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGGT GGGAGGAACC AGCTAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCCCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTT GTCATTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTG TTTTCAATAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACTTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA	60
ACTGGAGGGT ATTTATACCC AATTATCCC TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGT ATAACATTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG	240
TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGC TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC ATTAGAACGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGCCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCCTTTGC CAACAGGCCT	120
CCAAGTCAGG GCTGGGATTTC GTTCCCTTTG CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGCCTTCTGGGCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTCCATGT TTATAGCCTA GTT	173

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACCT TATCTCATCG AATTTTAAC CCAAACTCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTTCAT TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTGGCCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCCTGTC TCTAACCCCCA	300
TAGATTATNT CCAAATTCAAG TCAATTAAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCACAAATC ACCCCTTTAA TTACCATGCT ATGGTGG	477

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120
GATGATAAT AAGAGTCAGC CAGGTAAAGTG GGTGGGTGTGG TATGGGCACA GTGAAGAAC	180
TTTCAGGCAG AGGGAACAGC AGTGAAA	207

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG	60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGCG T	111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCAGA TACCTATCAT TACTCGATGC TGTTGATAAC	60
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT	120
GGATAACCAAC CGGAAACCC CTATCCCGCA CAGCCCAGTG TGGTCCCCAC TGTCTACGAG	180
GTGCATCCGG CTCAGT	196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC	60
CTTCCCTTT TCATCTAGTG GTGGAACCT GATGCTTAT GTTGACAGGA ATAGAACCGAG	120
GAGGGAGTTT GT	132

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAANACCCA NGANAGGCCA CTGGCCGTGG TGTCAATGCC	TCCAAACATG AAAGTGTAG	60
CTTCTGCTCT TATGTCTCA TCTGACAAC TCTTACCATT	TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTGGACT TGCCCTTGCG	TTGGAGGAAG TCATCAAACAC	180
CCTGGCTAGT GAGGGTGCAG CGCCGCTCCT GGATGACGGC	ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG	GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTTGGGCCA GGGCTTCATG ACCCTTTCTG	TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCCTTAAA TATCTTTAAC TGAAGGGGTC AGCCTCTGA	CTGCAAAGAC	120
CCTAACGCCGG TTACACAGCT AACTCCCCTG ATTGGCACAG	GGCCCTGATT TGTGAAATTG	180
GAGTCGAAGG TGTTCAGCTC CCCTCCTCCG ATGTTTACAA	CTGCTGCCTG	240
AGTTTACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT	TGAAACGAGA	300
GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG	CTCTGATTTG GAAATAAAAT CCGGAGAATG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG	60
GAAAGTGCCTT TGGGAACGT AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCCTCC TGGGCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT	240
GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGT AAGCAGCTG	300
GCCCTGGT	308

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACGTGA	120
GAATAGGAGA TTATGTTTGG CCCTCATATT CTCTCCTATC CTCCCTGCCT CATTCTATGT	180
CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTCAG AATAGAAAAC AAATTAACAG ACTAT	295

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTAA ATAGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGTA TATCTGTCCC	120
CTTAGT	126

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTCTGTG TGAGAAAATG	60
AANCCAGCAG GCTGCCCTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT	120
GCCTGGTAA TTCACCATT AATTCCCTCCC CCAAACCTCTC TGAGTCTTCC CTTAATATTT	180
CTGGTGGTTC TGACCAAAGC AGGTCAATGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA	240
NATTTTGTA GCCTTGATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGT	300
CCAACCTGT TTTCCCAAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGGA	360
NACAGACGGG CTCTTGCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG	420
TGTTCATCT CTGATGTCCT GT	442

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAC TG ATGGGTGACG TTGTAGGTT	60
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTTG ATTCCCTCACT ACAGGCCAAG GTTGTGGAAC TGGCANAAAG	180
GTGTGTTGTT GGANTTGAGC TCAGGGGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC	240
TGCTGTGGTG CGGGGANGTG AANGTGTGAG GTCACTTGAG CTTGGCCAGC TCTGGAAAGT	300
ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTA	360
CGAACCACTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTCA	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCNGCTGTG GAAGGTTGTA NATTGTCACC	480
AAGGAAATAA GCTGTGGT	498

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC	60
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT	120
GGAGCATGGC ATAGAGGAAG CTGANAAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC	180
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCA GATGCCTCTC	240
CCACCCCTTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTC TAACATCCTG	300
GAGAAAAATG GCAGTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA	360
CTTGTAGAAT GAAGCCTGGA	380

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA	60
CACTGTCCAC TGGCCCCCTTA TCCACTTGTT GCTTAATCCC TCGAAAGAGC ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAAA	60
GTTTTACTAC TCTGATAATT TTGTAACCA GGTAAACAGA ACATCCAGTC ATACAGCTTT	120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAAACCTAC TCACGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTATACA GACAGGCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATT CATACTTAAT GAGGGAGTTC CAGGAGATTC AACCAAGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACGT	180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTC TACACCTGTG	240
GGTTATGACA AAGACAACGT CCAAAGAACG AGGACTGCAA GTATATCGTG	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCCTAT CAGTAAAAG ATNTTGAGC AAACACTTT	469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CGGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACCTCG CCAAAGAATT	180
TTTGCAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCTTT TTGGTGAAC TTC	383

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

111

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTC	60
AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCACTGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC	180
AATTCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTTCTC CCCTGGAAAA CTCCAGCTTG	240
AGTCCCAGAT ACACCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG	180
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGCCATGG GCAAAGGCC C TACCACAAA AACAAATAGGA TCACTGCTGG GCACCAGCTC	300
ACGCACATCA CTGACAACCG GGATGAAAA AGAANTGCCA ACTTTCATAC ATCCAATGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGC CATCAGCTGC	420
TCGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTTGCCAACN CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAAG ATTGGAGTC TGGGAGGGGG AGTTGGGTG GGCATTTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA	TCATAAACGG	CGAGGACTGC	AGCCCGCACT	CGCAGCCCTG	GCAGGCGGCA	60
CTGGTCATGG	AAAACGAATT	GTTCTGCTCG	GGCGTCCTGG	TGCATCCGCA	GTGGGTGCTG	120
TCAGCCGCAC	ACTGTTTCCA	GAAGTGAGTG	CAGAGCTCCT	ACACCATCGG	GCTGGGCCTG	180
CACAGTCTTG	AGGCCGACCA	AGAGCCAGGG	AGCCAGATGG	TGGAGGCCAG	CCTCTCCGTA	240
CGGCACCCAG	AGTACAACAG	ACCCCTGCTC	GCTAACGACC	TCATGCTCAT	CAAGTTGGAC	300
GAATCCGTGT	CCGAGTCTGA	CACCATCCGG	AGCATCAGCA	TTGCTTCGCA	GTGCCCTACC	360
GCAGGGAACT	CTTGCCTCGT	TTCTGGCTGG	GGTCTGCTGG	CGAACGGCAG	AATGCCCTACC	420
GTGCTGCAGT	CGGTGAACGT	GTCGGTGGTG	TCTGAGGAGG	TCTGCAGTAA	GCTCTATGAC	480
CCGCTGTACC	ACCCCAGCAT	GTTCTGCGCC	GGCGGAGGGC	AAGACCAGAA	GGACTCCTGC	540
AACGGTGACT	CTGGGGGGCC	CCTGATCTGC	AAACGGGTACT	TGCAGGGCCT	TGTGTCTTTC	600
GGAAAAGCCC	CGTGTGGCCA	AGTTGGCGTG	CCAGGGTGTCT	ACACCAACCT	CTGCAAATTC	660
ACTGAGTGGA	TAGAGAAAAC	CGTCCAGGCC	AGTTAACTCT	GGGGACTGGG	AACCCATGAA	720
ATTGACCCCC	AAATACATCC	TGCGGAAGGA	ATTCAAGGAAT	ATCTGTTCCC	AGCCCTCCT	780
CCCTCAGGCC	CAGGAGTCCA	GGCCCCCAGC	CCCTCCTCCC	TCAAACCAAG	GGTACAGATC	840
CCCAGCCCC	CCTCCCTCG	ACCCAGGAGT	CCAGACCCCC	CAGCCCCCTCC	TCCCTCAGAC	900
CCAGGAGTCC	AGCCCCCTCC	CCCTCAGACC	CAGGAGTCCA	GACCCCCCAG	CCCCCTCCTCC	960
CTCAGACCCA	GGGGTCCAGG	CCCCCAACCC	CTCCTCCCTC	AGACTCAGAG	GTCCAAGCCC	1020
CCAACCCNTC	ATTCCCCAGA	CCAGAGGTC	CAGGTCCCAG	CCCCTCNNTCC	CTCAGACCCA	1080
GCGGTCCAAT	GCCACCTAGA	CTNTCCCTGT	ACACAGTGCC	CCCTTGTTGGC	ACGTTGACCC	1140
AACCTTACCA	GTTGGTTTTT	CATTTTTNGT	CCCTTTCCCC	TAGATCCAGA	AATAAAGTTT	1200
AAGAGAAGNG	CAAAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro
1				5				10					15		

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20 25 30
 Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 35 40 45
 Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 50 55 60
 Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
 65 70 75 80
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
 85 90 95
 Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
 100 105 110
 Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
 115 120 125
 Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
 130 135 140
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGCC	CTGGCAGGCG	GCACTGGTCA	TGGAAAACGA	ATTGTTCTGC	60
-TCGGCGTCC	TGGTGCATCC	GCAGTGGGTG	CTGTCAGCCG	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCCTTGCT	CGCTAACGAC	240
CTCATGCTCA	TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTCGC	AGTGCCCTAC	CGCGGGGAAC	TCTTGCCTCG	TTTCTGGCTG	GGGCTCTGCTG	360
GCGAACGGTG	AGCTCACGGG	TGTGTGTC	CCCTCTCAA	GGAGGTCTTC	TGCCCAGTCG	420
CGGGGGCTGA	CCCAGAGCTC	TGCGTCCCAG	GCAGAAATGCC	TACCGTGCTG	CAGTGCCTGA	480
ACGTGTCGGT	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCCGCTG	TACCACCCCCA	540
GCATGTTCTG	CGCGGGCGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCTGTAT	CTGCAACGGG	TACTTGCAGG	GCCTTGTGTC	TTTCGGAAAA	GCCCCGTGTG	660
GCCAAGTTGG	CGTGCAGGT	GTCTACACCA	ACCTCTGCAA	ATTCACTGAG	TGGATAGAGA	720

AAACCGTCCA GGCCAGTTAA CTCTGGGAC TGGGAACCA TGAAATTGAC CCCCAAATAC	780
ATCCTGCGGA AGGAATTCA GAAATATCTGT TCCCAGCCCC TCCTCCCTCA GGCCAGGAG	840
TCCAGGCCCC CAGCCCCCTCC TCCCTCAAAC CAAGGGTACA GATCCCCAGC CCCTCCTCCC	900
TCAGACCCAG GAGTCCAGAC CCCCCAGCCC CTCCCTCCCTC AGACCCAGGA GTCCAGCCCC	960
TCCTCCNTCA GACCCAGGAG TCCAGACCCC CCAGCCCCCTC CTCCCTCAGA CCCAGGGGTT	1020
GAGGCCCCCA ACCCCCTCCTC CTTCAGAGTC AGAGGTCAA GCCCCCAACC CCTCGTTCCC	1080
CAGACCCAGA GGTNNAGGTC CCAGCCCCCTC TTCCNTCAGA CCCAGNGGTC CAATGCCACC	1140
TAGATTTTCC CTGNACACAG TGCCCCCTTG TGGNANGTTG ACCAACCTT ACCAGTTGGT	1200
TTTTCATTTT TNGTCCCTTT CCCCTAGATC CAGAAATAAA GTTTAAGAGA NGNGCAAAAA	1260
AAAAAA	1265

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC ACACTGTTTC CAGAAGTGAG TGCAGAGCTC CTACACCATC GGGCTGGGCC	60
TGCACAGTCT TGAGGCCGAC CAAGAGCCAG GGAGGCCAGAT GGTGGAGGCC AGCCTCTCCG	120
TACGGCACCC AGAGTACAAC AGACCCCTTGC TCGCTAACGA CCTCATGCTC ATCAAGTTGG	180
ACGAATCCGT GTCCGAGTCT GACACCATCC GGAGCATCAG CATTGCTTCG CAGTGCCTTA	240
CCGGGGGAA CTCTTGGCTC GGGGTCTGCT GGCGAACGGT GAGCTCACGG	300
GTGTGTGTCT GCCCTCTTCA AGGAGGTCT CTGCCCAGTC GCGGGGGCTG ACCCAGAGCT	360
CTGCGTCCCA GGCAGAAATGC CTACCGTGT GCAGTGCCTG AACGTGTCGG TGGTGTCTGA	420
NGAGGTCTGC ANTAAGCTCT ATGACCGCT GTACCACCCC ANCAGTTCT GCGCCGGCGG	480
AGGGCAAGAC CAGAAGGACT CCTGCAACGT GAGAGAGGGG AAAGGGGAGG GCAGGGGACT	540
CAGGGAAGGG TGGAGAAGGG GGAGACAGAG ACACACAGGG CCGCATGGCG AGATGCAGAG	600
ATGGAGAGAC ACACAGGGAG ACAGTGACAA CTAGAGAGAG AAACTGAGAG AAACAGAGAA	660
ATAAACACAG GAATAAAAGAG AAGCAAAGGA AGAGAGAAC AGAAAACAGAC ATGGGGAGGC	720
AGAAAACACAC ACACATAGAA ATGCAGTTGA CCTTCCAACA GCATGGGGCC TGAGGGCGGT	780
GACCTCCACC CAATAGAAAA TCCTCTTATA ACTTTTACT CCCCAAAAC CTGACTAGAA	840
ATAGCCTACT GTTGACGGGG AGCCTTACCA ATAACATAAA TAGTCGATTT ATGCATACGT	900
TTTATGCATT CATGATATAC CTTTGTGGA ATTITTTGAT ATTTCTAAGC TACACAGTTTC	960
GTCTGTGAAT TTTTTAAAT TGTTGCAACT CTCCCTAAAT TTTTCTGATG TGTGTTATTGA	1020
AAAAATCCAA GTATAAGTGG ACTTGTGCAT TCAAACCAAGG GTTGTCAAG GGTCAACTGT	1080
GTACCCAGAG GGAAACAGTG ACACAGATTG ATAGAGGTGA AACACGAAGA GAAACAGGAA	1140
AAATCAAGAC TCTACAAAGA GGCTGGGCAG GTTGGCTCAT GCCTGTAATC CCAGCACTTT	1200
GGGAGGGCGAG GCAGGCAGAT CACTTGAGGT AAGGAGTTCA AGACCAGCT GGCCAAAATG	1260
GTGAAATCCT GTCTGTACTA AAAATACAAA AGTTAGCTGG ATATGGTGGC AGGCGCCTGT	1320
AATCCCAGCT ACTTGGGAGG CTGAGGCAGG AGAATTGCTT GAATATGGGA GGCAGAGGTT	1380
GAAGTGAGTT GAGATCACAC CACTATACTC CAGCTGGGGC AACAGAGTAA GACTCTGTCT	1440
CAAAAAAAAAA AAAAAAAAAA	1459

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GC	GCAGCCCT	GGCAGGCGGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGGCGTCCTG	60
GT	GCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTCC	AGAACTCCTA	CACCATCGGG	120
CT	GGGCCTGC	ACAGTCTTGA	GGCCGACCAA	GAGCCAGGGA	GCCAGATGGT	GGAGGCCAGC	180
CT	CTCCGTAC	GGCACCCAGA	GTACAACAGA	CTCTTGCTCG	CTAACGACCT	CATGCTCATC	240
AAGTGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGCAG	300	
TGCCCTACCG	CGGGGAACCTC	TTGCCTCGTN	TCTGGCTGGG	GTCTGCTGGC	GAACGGCAGA	360	
ATGCCTACCG	TGCTGCACTG	CGTGAACTGTG	TCGGTGGTGT	CTGAGGANGT	CTGCAGTAAG	420	
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCAGAAG	480	
GACTCCTGCA	ACGGTGAAC	TGGGGGCC	CTGATCTGCA	ACGGGTACTT	GCAGGGCCTT	540	
GTGTCTTCG	GAAAAGCCCC	GTGTGGCCAA	CTTGGCGTGC	CAGGTGTCTA	CACCAACCTC	600	
TGCAAATTCA	CTGAGTGGAT	AGAGAAAACC	GTCAGNCCA	GTAACTCTG	GGGACTGGGA	660	
ACCCATGAAA	TTGACCCCCA	AATAACATCCT	GCGGAANGAA	TTCAGGAATA	TCTGTTCCC	720	
GCCCCTCCTC	CCTCAGGCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCTCCCT	CAAACCAAGG	780	
GTACAGATCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCC	AGCCCCCTCNT	840	
CCNTCAGACC	CAGGAGTCCA	GCCCCCTCCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900	
CCNTCNTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TCNTCCNTCA	GAGTCAGAGG	960	
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAGC	CCCTCCTCCC	1020	
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCC	CCTTGTGGCA	1080	
NGTTGACCCA	ACCTTACCA	TTGGTTTTTC	ATTTTTGTC	CCTTTCCCT	AGATCCAGAA	1140	
ATAAAGTNTA	AGAGAAGCGC	AAAAAAA				1167	

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10			15			

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
				20				25				30			

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
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Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu	50	55
-----------------------------------------------------------------	----	----

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser	65	70
-----------------------------------------------------------------	----	----

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly	85	90
-----------------------------------------------------------------	----	----

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met	100	105
-----------------------------------------------------------------	-----	-----

Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val	115	120
-----------------------------------------------------------------	-----	-----

Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala	130	135
-----------------------------------------------------------------	-----	-----

Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly	145	150
-----------------------------------------------------------------	-----	-----

Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys	165	170
-----------------------------------------------------------------	-----	-----

Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys	180	185
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Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser	195	200
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205

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC AGCCCTGGCA GGCAGGCACTG GTCATGGAAA ACGAATTGTT CTGCTCGGGC	60
GTCTCTGGTGC ATCCGCAGTG GGTGCTGTCA CCCGCACACT GTTTCCAGAA CTCCTACACC	120
ATCGGGCTGG GCCTGCACAG TCTTGAGGCC GACCAAGAGC CAGGGAGCCA GATGGTGAG	180
GCCAGCCTCT CGGTACGGCA CCCAGAGTAC AACAGACCCCT TGCTCGCTAA CGACCTCATG	240
CTCATCAAGT TGGACGAATC CGTGTCCGAG TCTGACACCA TCCGGAGCAT CAGCATTGCT	300
TCGCAGTGCC CTACCGCGGG GAACTCTTGC CTCGTTTCTG GCTGGGGTCT GCTGGCGAAC	360
GATGCTGTGA TTGCCATCCA GTCCCAGACT GTGGGAGGCT GGGAGTGTGA AAAGCTTTCC	420
CAACCCTGGC AGGGTTGTAC CATTCCGGCA ACTTCCAGTG CAAGGACGTC CTGCTGCATC	480

CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGGAA CACTGTGATC AACTAGCCAG	540
CACCATAGTT CTCCGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGTCTATTGT	600
ACTAACCATG CCGATGTTA GGTGAAATTG GCGTCACTTG GCCTCAACCA TCTTGGTATC	660
CAGTTATCCT CACTGAATTG AGATTCCTG CTTCAGTGTG AGCCATTCCC ACATAATTTC	720
TGACCTACAG AGGTGAGGGG TCATATAGCT CTTCAAGGGAT GCTGGTACTC CCCTCACAAA	780
TTCATTTCTC CTGTTGTAGT GAAAGGTGCG CCCTCTGGAG CCTCCCAGGG TGGGTGTGCA	840
GGTCACAATG ATGAATGTAT GATCGTGTTC CCATTACCCA AAGCCTTAA ATCCCTCATG	900
CTCAGTACAC CAGGGCAGGT CTAGCATTTC TTCATTTAGT GTATGCTGTG CATTCATGCA	960
ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG CCTCCTGGG	1020
GAGGTGAGGG AGAGGGCCCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA CATTAGGTGC	1080
TTAATAAACAA GAAGCTGTGA TGTTAAAAAA AAAAAAAA	1119

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Glu	Asn	Glu	Lieu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5						10					15

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
							20			25					30

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
				35				40						45	

Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu
					50			55						60	

Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
				65		70				75					80

Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
					85				90					95	

Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Asp	Ala	Val
				100				105						110	

Ile	Ala	Ile	Gln	Ser	Xaa	Thr	Val	Gly	Gly	Trp	Glu	Cys	Glu	Lys	Leu
					115				120					125	

Ser	Gln	Pro	Trp	Gln	Gly	Cys	Thr	Ile	Ser	Ala	Thr	Ser	Ser	Ala	Arg
				130				135						140	

Thr	Ser	Cys	Cys	Ile	Leu	Thr	Gly	Cys	Ser	Leu	Leu	Thr	Ala	Ser	
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145

150

155

160

Pro Gly Thr Leu

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCC CCGGCCGGGG GATGCGAGGC TCGGAGCACC CTTGCCCGC TGTGATTGCT	120
GCCAGGCACT GTTCATCTCA GCTTTCTGT CCCTTGCTC CCGGCAAGCG CTTCTGCTGA	180
AAGTTCATAT CTGGAGCCTG ATGTCTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAAA	240
AAAAAAAAAAA	250

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACAA	60
TCACCCAGAC CCCGCCCTG CCCGTGCCAC ACGCTGCTGC TAACGACAGT ATGATGCTTA	120
CTCTGCTACT CGGAAACTAT TTTTATGTAA TTAATGTATG CTTTCTGTT TATAATGCC	180
TGATTTAAAA AAAAAAAAAA AA	202

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG	60
AATGTTAGG CAGTGCTAGT AATTCTYTCG TAATGATTCT GTTATTACTT TCCTNATTCT	120
TTATTCCCTCT TTCTTCTGAA GATTAATGAA GTTAAAATT GAGGTGGATA AATACAAAAAA	180
GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA	240
AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTATAT GCTGTTGAAC	300
CTACTCTGTT CCTTGGCTAG AAAAATTAT AACACAGGACT TTGTTAGTTT GGGAGCCAA	360
ATTGATAATA TTCTATGTTA TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW	420

TTTTATTCCC AGGAATATGG KGTCATTT ATGAATATTA CSCRGGATAG AWGTWTGAGT	480
AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTC	540
CAAAAAAAA AAAAAAAA	558

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTK GRGGATGCTA AGSCCCCRGA RWTYGTTTGA TCCAACCCTG GCTTWTTTTC	60
AGAGGGGAAA ATGGGGCCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG	120
CSTCACACAG ASTCCCGAGT AGCTGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG	180
TTWGCAATTG ACGTTGCCAC CTCCAACCTTA AACATTCTTC ATATGTGATG TCCTTAGTCA	240
CTAAGGTTAA ACTTTCCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTCA	300
TACTMTTCTA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGGTT GATAGGAANT	360
NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTGG TACGCATARA	420
AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAA ARAAAAAAAA AAAAAAAA	479

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC AGAACGCTAAA GCCAAAGCCC AAGAACAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAG TGCCAGTGCC AGTGCCAGCA CCAGTGGTGG CTTCAGTGCT	120
GGTGCCAGCC TGACCGCCAC TCTCACATTG GGGCTCTTCG CTGGCCTTGG TGGAGCTGGT	180
GCCAGCACCA GTGGCAGCTC TGGTGCCTGT GGTTTCTCCT ACAAGTGAGA TTTTAGATAT	240
TGTTAACCTT GCCAGTCTTT CTCTTCAAGC CAGGGTGCAT CCTCAGAAAC CTACTCAACA	300
CAGCACTCTA GGCAAGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATTT	360
GCCATTCAA AAAAAAAA AAAA	384

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYYNT CCRGTATKAC CTCAACGAGC	60
-------------------------------------------------------------------	----

AGGGAGATCG AGTCTATAACG CTGAAGAAAT TTGACCCGAT GGGACAACAG ACCTGCTCAG	120
CCCATCCTGC TCGGTTCTCC CCAGATGACA AATACTCTSG ACACCGAAC ACCATCAAGA	180
AACGCTTCAA GGTGCTCATG ACCCAGCAAC CGCGCCCTGT CCTCTGAGGG TCCCTTAAAC	240
TGATGTCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAACCT CTTCGGACTG	300
TGAGCCCTGA TGCCCTTTTG CCAGCCATAC TCTTGGCAT CCAGTCTCTC GTGGCGATTG	360
ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCCATA AAGGGAACAC ATTTGACTTT	420
TTTTCTCAT ATTTAAATT ACTACMAGAW TATTWMAGAW WAAATGAWT T GAAAAACTST	480
TAAAAAAAAA AAAAAA	496

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGACTTCC	60
CAAGTATCYT GCGCGCGTC TTCTACCGTC CCTACCTGCA GATCTTCGGG CAGATCCCC	120
AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAACTG YTCGTGGAG CCCGGCTTCT	180
GGGCACACCCC TCCTGGGGCC CAGGGGGCA CCTGCGTCTC CCAGTATGCC AACTGGCTGG	240
TGGTGCTGCT CCTCGTCATC TTCTGCTCG TGGCCAACAT CCTGCTGGTC AACTTGCTCA	300
TGCCATGTT CAGTTACACA TTCGGCAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG	360
GCGCAGCGTT ACCGCCTCAT CCGG	384

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 577 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCCTCTCGC TTCAACCGC	60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CYTCCTGGCA TCTTGGGGCG GCNTAATATT	120
CCAGGAAACT CTCAAATCAAG TCACCGTCGA TGAAACCTGT GGGCTGGTTC TGTCTCCGC	180
TGGGTGTGAA AGGATCTCCC AGAAGGAGTG CTCGATCTTC CCCACACTTT TGATGACTTT	240
ATTGAGTCGA TTCTGCATGT CCAGCAGGAG GTTGTACCAAG CTCTCTGACA GTGAGGTCAC	300
CAGCCCTATC ATGCCGTGTA MCGTGGCAA GARCACCGAG CCTTGTGTGG GGGKKGAAGT	360
CTCACCCAGA TTCTGCATTA CCAGAGAGCC GTGGAAAAG ACATTGACAA ACTCGCCAG	420
GTGGAAAAG AMCAMCTCCT GGARGTGTCTN GCGGCTCCTC GTCMGTGGT GGCAGCGCTW	480
TCCCTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGCCC CCAGAAANTT GTCATCATCC	540
AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAAT	577

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCGSGTG	AGAATYCATW	60
ACTKGGAAAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTCAACAT	ATGCAACACT	120
TTAACACAGTG	TGTCAATCTG	CTCCCCYNAC	TTTGTCATCA	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATTIC	ACACCTGTTA	AAAGGGCGCT	AAGCATTITIT	GATTCAACAT	CTTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTTATYAT	TTGTTAGCCA	ATTCACTTTTC	300
TTCATGGGAC	AGAGCCATYT	GATTAAAAAA	GCAAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTGGA	GCGGAAGAGT	AGCCTTCTA	CTTCACCAGA	CACAACCTCCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTAA	CCACTTGCAC	AAGAAGGCCT	TTTCTCCTC	AGGC	534

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCAGT	ATCTCTNAAA	ACAAACCTCTC	ATACCTTGTG	GACCTAATT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTT	TACTTTGTA	AAAGCTTATG	120
CCTCTTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGCTCTCTG	TGTAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCAGATN	ACAACACTNA	CAAACCTCTC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACATWA	CCTGGTGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAA	RMGTTWTKTT	WTTCCTCCCTT	420
GCAAAAAACA	TGTACNGACT	TCCCCTTGAG	TAATGCCAAG	TTGTTTTTT	TATNATAAAA	480
CTTGCCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCCTAACAA	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTTCATTA	AAAATGTTG	CTAAATACAA	CTTGAACTA	660
TTTTCTGTN	TTCCCAGAGC	TGAGATNTA	GATTTATGT	AGTATNAAGT	AAAAANTAC	720
GAAAATAATA	ACATTGAAGA	AAAANANAAA	AAANAAAAAA	A		761

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT	TTTGCCGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCCTG	CTGAGCAACA	120
AAGCCGCCTG	CTGCCTTCTC	TGTCTGTCTC	CTGGTGCAGG	CACATGGGGA	GACCTTCCCC	180

AAGGCAGGGG CCACCAGTCC AGGGGTGGGA ATACAGGGGG TGGGANGTGT GCATAAGAAG	240
TGATAGGCAC AGGCCACCG GTACAGACCC CTCGGCTCCT GACAGGTNGA TTTCGACCAG	300
GTCATTGTGC CCTGCCAGG CACAGCGTAN ATCTGGAAA GACAGAATGC TTTCCCTTTC	360
AAATTTGGCT NGTCATNGAA NGGGCANTTT TCCAANTTNG GCTNGGTCTT GGTACNCTTG	420
GTTCGGCCA GCTCCNCCTC CAAAAANTAT TCACCCNNCT CCNAATTGCT TGCGNGNCCC	480
CC	482

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT TTTTAAACA GTTTTCACA ACAAAATTAA TTAGAAGAAT AGTGGTTTTG	60
AAAACACTCG CATCCAGTGA GAACTACCAT ACACCACATT ACAGCTNGGA ATGTNCTCCA	120
AATGTCTGGT CAAATGATAC AATGGAACCA TTCAATCTTA CACATGCACG AAAGAACAG	180
CGCTTTGAC ATACAATGCA CAAAAAAAAGGGGGGGGG GACCACATGG ATTAAAATT	240
TAAGTACTCA TCACATACAT TAAGACACAG TTCTAGTCCA GTCNAAAATC AGAACTGCNT	300
TGAAAAAATT CATGTATGCA ATCCAACCAA AGAACTTNAT TGGTGATCAT GANTNCTCTA	360
CTACATCNAC CTTGATCATT GCCAGGAACN AAAAGTTNAA ANCACNCNGT ACAAAAANAA	420
TCTGTAATTN ANTTCAACCT CCGTACNGAA AAATNTTNNT TATACACTCC C	471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA AGGTCTGTTT TASTGTCGGM CTGTTCAGCC ACCAACTCTA ACAAGTTGCT	60
GTCTTCCACT CACTGTCTGT AAGCTTTTA ACCCAGACWG TATCTTCATA AATAGAACAA	120
ATTCTTCACC AGTCACATCT TCTAGGACCT TTTGGATTTC AGTTAGTATA AGCTCTTCCA	180
CTTCCTTTGT TAAGACTTCA TCTGGTAAAG TCTTAAGTTT TGTAGAAAGG AATTYAATTG	240
CTCGTTCTCT AACAAATGTCC TCTCCTTGAA GTATTTGGCT GAACAACCCA CCTAAAGTCC	300
CTTTGTGCAT CCATTTAAA TATACTTAAT AGGGCATTGK TNCACTAGGT TAAATTCTGC	360
AAGAGTCATC TGTCTGCAAA AGTTGCGTTA GTATATCTGC CA	402

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TTGTC TGAGGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	120
ATGCYTYTTT	GAYTACCGTG	TGCAAGTGC	TGGTGATTCT	YAAACACACYT	180
CTTTTGTGGA	AAAACGTGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGCAATT	GCTTTTGTC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTGCC	TCCATCACAT	TTGTGATCTG	360
TACATCTCCT	GACAGTA CTG	AAGAACTTCT	TCTTTTGTTT	CAAAGCARC	420
TGTGGATCA	GGTTCC CATT	TCCCAGTCYG	AATGTTCA CA	TGGCATATT	480
AAAACATTGC	GATTTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	600
G					601

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCA	NATCCCACCA	CGAAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACGCAG	GCAGMAGCGG	GSCCGGTCAA	TGAACCTCCAY	TCGTGGCTTG	GGGTTKGACGG	180
TKAAGTGCAG	GAAGAGGCTG	ACCACCTCGC	GGTCCACCAG	GATGCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCAG	GGCCTTGCCC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GCCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCAGTG	TGTCGCGCTC	420
CAGGAMMGSC	ACCAGCGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGT	TTTGTGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTCGCGCCTG	CGTGAGCAGC	ATGAAGGCAGT	TGTCGGCTCG	CAGTTCTTCT	TCAGGAACTC	600
CACGCAAT					608	

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGCCTCAA	TGCAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTC CAAAC	240
AAACAACAACA	AAATAACATG	TTTGCCTGTT	AAAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TIGCAATTTC	TGTATTATT	GKTNCTSTGG	360
AAATAAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTC	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GTYTCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAGGC	CCCATTCCCG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCACAGACACC	CCTTCACCTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCTCTCA	GTCCCTTCC	STACACCTG	AMCGGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGGAR	TGTGCTCAAG	GARTCGCNGG	420
GCARCGTGG	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAAA	AAAAANAAAAA	AA				502

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCAT	TTGTCCTGCTC	60
CCTCTGGAAG	CCTTGGCCAG	ACCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATT	120
WAGCTGTTK	GAGTTGATT	GCACCACTGC	ACCCACAAC	TCAATATGAA	AACYAWTTGA	180
ACTWATTTAT	TATCTTGTGA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTKATC	240
AAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTAAATTAT	GATTGCCATT	300
ATTAATCGGC	AAAATGTGGA	GTGTATGTT	TTTCACAGT	AATATATGCC	TTTGTAAC	360
TCACTTGGTT	ATTTTATTGT	AAATGARTTA	CAAAATTCTT	AATTTAAGAR	AATGGTATGT	420
WATATTATT	TCATTAATT	CTTTCCTKGT	TTACGTTAAT	TTGAAAAGA	WTGATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAGTAGTTG	ACCCACATCC	CTATGACTTT	540
TTCTTACAAT	GTATAAAAGGT	TGTAGCCAT	CNAACTTCAA	AGAAAAAAAT	GACCACATAC	600
TTTGCATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTTATAA	ACTAGCAAAN	660
	AAGTG					665

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTTT	TTTTTTTGC	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTATAA	NATTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTT	ACCTCGTANA	GATNACAGAC	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTTCAA	AAGATTAAT	CCAAACTGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTTCT	GAACTTTAGA	TTTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTIT	GTTCATNCTG	480
ANCNTGGCTT	AA					492

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTTGN	ATTCANTCT	GTANNAANTA	TTTCATTAT	GTTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACINTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATTT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNIGTAG	300
GAGTTGTGGC	TTTATGTTTA	CTGAAAGTCA	ATGCAGTTCC	I GTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAAATT	TGATNCAA	478

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTTCAG	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCA GCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTNNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAAAT	ACCACATGTN	TGTNGTATCC	TGGTGCNNG	CCGTTTANTG	420
AACNTNGACN	NCACCCTTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCT	GCTCCTCTGC	480
GA						482

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGGGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGCG	GCGACAGTCG	CAGGTGCAGC	GCGGGCCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCGCA	GAGGTGCGTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCCGT	GAANGCGGGA	GGCCTCGGGG	AGCCCTCGG	GAAGGGCGGC	240
CCGAGAGATA	CGCAGGTGCA	GGTGGCCGCC				270

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTCTGTGG	120
TTGATTGGTT	TGTCTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCGAACG	ANAANTAAACA	180
TGGAGTGGGT	GCACCCCTCCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACCTGG	240
TCTGTGACCG	TCATTTTCTT	GACATCAATG	TTATTAGAAG	TCAGGATATC	TTTTAGAGAG	300
TCCAATGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCCAANA	TCCAANCAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TGGCACTTAA	TCCATTTTA	TTTCAAAATG	TCTACAAANT	TTNAATNCNC	CATTATAACNG	120
GTNATTTTNC	AAAATCTAAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNNAA	180
TACNCNCAAA	AATCAAAAAT	ATACNTNTCT	TTCAGCAAC	TTNGTTACAT	AAATTAAAAAA	240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTAA	CACTGCAAAC	ATNTTTNNAA	300
GGAACAAAAA	TAAAAAAAAA	CACTNCCGCA	AAGGTAAAG	GGAACAAACAA	ATTCTNTTTA	360
CAACANCNC	NATTATAAAA	ATCATATCTC	AAATCTTAGG	GGAATATATA	CTTCACACNG	420
GGATCTTAAC	TTTIACTNCA	CTTTGTTTAT	TTTTTANAA	CCATTGTNTT	GGGCCAACA	480
CAATGGNAAT	NCCNCCNCNC	TGGACTAGT				509

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTTT	TTTTTTTTG	CCCCCCTCTT	ATAAAAAAACA	AGTTACCATT	TTATTTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTTT	AAAATCAAAC	I20
TAAATGGAAA	CTGCCCTAGA	TACATAATT	TTAGGAATT	GCTTAAAATC	TGCCCTAAAGT	I80
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAAAAC	ATCCAAATTC	240
ATTTTTCTTG	TCTTTAAAAT	TATCTAATCT	TTCCATT	TCCCTATTCC	AAGTCAATT	300
GCTTCTCTAG	CCTCATT	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAAA	360
AGGGAAAACA	GGAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTCTACC	420
TACGTTAATA	AAATAGCATT	TTGTAAGGC	AGCTAAAAG	AAGGCTTAGA	TCCTTTATG	480
TCCATT	TCACTAAACG	ATATCNAAG	TGCCAGAATG	CAAAGGTTT	GTGAACATTT	540
ATTCAAAAGC	TAATATAAGA	TATTCACAT	ACTCATCTT	CTG		583

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTNTT	TTTTTNCTC	TTCTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAAA	CTCATCTTC	CAGCTTTAAA	ATAACAATCA	I20
AATCTCTTAT	GCTATATCAT	ATTTAAGTT	AAACTAATGA	GTCACTGGCT	TATCTCTCC	I80
TGAAGGAAAT	CTGTTCATTC	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	CCTTGCATAT	240
TGAGAGGTTT	TTCTTCTCTA	TTTACACATA	TATTCCATG	TGAATTGT	TCAAACCTTT	300
ATTTTCATGC	AAACTAGAAA	ATAATGTNTT	CTTTGCATA	AGAGAAGAGA	ACAATATNAG	360
CATTACAAAA	CTGCTCAAAT	TGTTGTTAA	GNTTATCCAT	TATAATTAGT	TNGGCAGGAG	420
CTAACATACAA	TCACATTAC	NGACNAGCAA	TAATAAAACT	GAAGTACCA	TTAAATATCC	480
AAAATAATT	AAGGAACATT	TTTAGCCTGG	GTATAATTAG	CTAATTCACT	TTACAAGCAT	540
TTATTNAGAA	TGAATTACA	TGTTATTATT	CCNTAGCCCCA	ACACAATGG		589

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTNTTTT TTTTTCAGT AATAATCAGA ACAATATTAA TTTTTATATT TAAAATTCA	60
AGAAAAGTGC CTTACATTAA ATAAAAGTTT GTTTCTCAA GTGATCAGAG GAATTAGATA	120
TNGTCTTGAA CACCAATAATT AATTGAGGA AAATACACCA AAATACATTA AGTAAATTAT	180
TTAAGATCAT AGAGCTTGTA AGTAAAAGA TAAAATTGA CCTCAGAAC TCTGAGCATT	240
AAAAATCCAC TATTAGCAAA TAAATTACTA TGAGCTTCTT GCTTAAATT TGTGATGAA	300
ATGGGGTGTGTC ACTGGTAAAC CAACACATTC TGAGGATAC ATTACCTAGT GATAGATTCT	360
TATGTAATTGCTT GCTANATNAC GTGGATATGA GTTGACAAGT TTCTCTTCT TCAATCTTT	420
AAGGGCGNGA NGAAATGAGG AAGAAAAGAA AAGGATTACG CATACTGTT TTTCTATNGG	480
AAGGATTAGA TATGTTCTT TTGCCAATAT TAAAAAAATA ATAATTTA CTACTAGTGA	540
AACCC	545

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTTT TTTTTTAGTC AAGTTCTNA TTTTTATTAT AATTAAAGTC TTGGTCATT	60
CATTATTAG CTCTGCAACT TACATATTAA AATTAAAGAA ACGTINTTAG ACAACTGTNA	120
CAATTATATAA ATGTAAGGTG CCATTATTGA GTANATATAT TCCTCCAAGA GTGGATGTGT	180
CCCTTCTCCC ACCAACTAAT GAANCAGCAA CATTAGTTA ATTTTATTAG TAGATNATAC	240
ACTGCTGCAA ACGCTAATTC TCTTCTCCAT CCCCATGTNG ATATTGTGTA TATGTGTGAG	300
TTGGTNAGAA TGATCANCA ATCTNACAAT CAACAGCAAG ATGAAGCTAG GCNTGGGCTT	360
TCGGTAAAAA TAGACTGTGT CTGCTGAAT CAAATGATCT GACCTATCCT CGGTGGCAAG	420
AACTCTTCGA ACCGCTCCT CAAAGGCNGC TGCCACATT GTGGCNTCTN TTGCACTTGT	480
TTCAAAA	487

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT AAAAGACTGC ATTTTANAA CTAGCAACTC TTATTTCTTT CCTTTAAAAA	60
TACATAGCAT TAAATCCAA ATCCTATTAA AAGACCTGAC AGCTTGAGAA GGTCACTACT	120
GCATTTATAG GACCTTCTGG TGGTTCTGCT GTTACNTTG AANTCTGACA ATCCTTGANA	180
ATCTTTGCAT GCAGAGGAGG TAAAAGGTAT TGGATTTCAGAGGAANA ACACAGCGCA	240
GAAATGAAGG GGCCAGGCTT ACTGAGCTG TCCACTGGAG GGCTCATGGG TGGGACATGG	300
AAAAGAAGGC AGCCTAGGCC CTGGGGAGCC CA	332

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GCGGAGGGCG	TTACTGTITI	GTCTCAGTAA	CAATAAATAC	AAAAAGACTG	60
GTGTTGTTCC	GGCCCCATCC	AACCACGAAG	TTGATTTC	TTGTGTGCAG	AGTGACTGAT	120
TTAAAGGAC	ATGGAGCTTG	TCACAAATGTC	ACAATGTCAC	AGTGTGAAGG	GCACACTCAC	180
TCCCGCGTGA	TTCACATTAA	GCAACCAACA	ATAGCTCATG	AGTCCATACT	TGTAAATACT	240
TTTGGCAGAA	TACTTNTTGA	AACTTGCAGA	TGATAACTAA	GATCCAAGAT	ATTCCCAAA	300
GTAAATAGAA	GTGGGTCTATA	ATATTAAATTAA	CCTGTTACA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGCCCAG	ACACTGACAT	CAAACTAAGC	CCACTTAGAC	TCCTCACCA	CAGTCTGTCC	420
TGTCATCAGA	CAGGAGGCTG	TCACCTTGAC	CAAATTCTCA	CCAGTCAATC	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCCGGTAATG	CACCACCTTG	GTGA		524

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA	ATCCAGAGTT	GCCATGGAGA	AAATTCCAGT	GTCAGCATTC	TTGCTCCTTG	60
TGGCCCTCTC	CTACACTCTG	GCCAGAGATA	CCACAGTCAA	ACCTGGAGCC	AAAAAGGACA	120
CAAAGGACTC	TCGACCCAAA	CTGCCCGAGA	CCCTCTCCA			159

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC	AGACAAAGGC	AGAGGGAGAGA	GCTCTGTTAG	TTCTGTGTTG	TTGAACTGCC	60
ACTGAATTTC	TTTCCACTTG	GACTATTACA	TGCCANTGAA	GGGACTAATG	GAAAAACGTA	120
TGGGGAGATT	TTANCCAATT	TANGTNTGTA	AATGGGGAGA	CTGGGGCAGG	CGGGAGAGAT	180
TTGCAGGGTG	NAAATGGGAN	GGCTGGTTG	TTANATGAAC	AGGGACATAG	GAGGTAGGCA	240
CCAGGATGCT	AAATCA					256

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA	180
GGGGAGATAC ATTNCNGAAAG AGGACTGAAA GAAATACTCA AGTNGAAAAA CAGAAAAAGA	240
AAAAAAAGGAG CAAATGAGAA GCCT	264

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAAA	60
GGATTTAATG TTGTCTCAGC TTGGGCACCT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG	120
GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCGCCAG	180
TTNAATTTC TTCCCATTGA CTTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTAA	240
CCCCTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA	300
TTTTTTTTTC CTTTATTCCCT TTGTCAGA	328

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AAACTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT	240
TCTCATCGGT	250

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAACAT	CAATGCTGAA	TATTTGGCTT	CATTATTCCC	AGATTCTTG	ATTGTCAAAG	60
GATTTAATGT	TGTCTCAGCT	TGGGCACTTC	AGTTAGGACC	TAAGGATGCC	AGCCGGCAGG	120
TTTATATATG	CAGCAACAAT	ATTCAAGCGC	GACAACAGGT	TATTGAACCT	GCCCCGCCAGT	180
TGAATTTCAT	TCCCATTGAC	TTGGGATCCT	TATCATCAGC	CANAGAGATT	GAAAATTAC	240
CCCTACGACT	CTTTACTCTC	TGGAGAGGGC	CAGTGGTGGT	AGCTATAAGC	TTGGCCACAT	300
TTTTTTTCTC	TTTATTCCTT	TGTCAGAGAT	GCGATTACATC	CATATGCTAN	AAACCAACAG	360
AGTGAACCTT	ACAAAATTCC	TATAGANATT	GTGAATAAAA	CTTACCTAT	AGTTGCCATT	420
ACTTTGCTCT	CCCTAATATA	CCTC				444

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC	AGAGCGACAT	ATCCAAGTGT	ANACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTTCAAT	TCTCCAAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAAGC	CATGTTGAGA	AACAAATATC	TCTCTGACCT	240
TCTCATCGGT	AAGCAGAGGC	TGTAGGCAAC	ATGGACCATA	GCGAANAAAA	AACTTAGTAA	300
TCCAAGCTGT	TTTCTACACT	GTAACCGAGT	TTCCAACCAA	GGTGAAATC	TCCTATACTT	360
GGTGCC						366

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC	AGAACTCCAC	TGCANGAGGG	AGGGCCGGGC	CAGGAGAACAT	TCCGCTTGTC	60
CAAGACAGGG	GCCTAAGGAG	GGTCTCCACA	CTGCTNNTAA	GGGCTNTTNC	ATTTTTTTAT	120
TAATAAAAAG	TNNAAAAGGC	CTCTTCTCAA	CTTTTTTCCC	TTNGGCTGGA	AAATTTAAAA	180
ATCAAAAATT	TCCTNAAGTT	NTCAAGCTAT	CATATATACT	NTATCCTGAA	AAAGCAACAT	240

AATTCTTCCT TCCCTCCTT

260

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCCTAT AATTTCTAT TTTAATAAGG AAATAGCAA TTGGGGTGGG GGGAAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAAATTTT	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCTA	240
ATATCCTTCA TGCTTGTAAA GT	262

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	93

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCCT TCATCTTGA TTCCATGAGG	60
TCTTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC	60
GTTCTTCACC TGTCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAGGA TGGATGAAAA AAATTAATAA TGAATTTTG CATAATCCAA	180
TTTCTCTTT TATATTTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGAAATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTTGAGT	300
CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T	351

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTAA ATWRTRTTK GTGGCATTTC CTTACATTGT CTTGACAAGA	120
TTAAATGTC TGTGCCAAA TTTTGTATTT TATTTGGAGA CTICITATCA AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATT	240
TAAAAGATTT TGATTTCTG GAATGACAAT TATATTTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTGTTG	360
ACCATTAAGC TATATGTTA AAA	383

(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCCTGAAGG CTTCTTGTAA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:

(a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.

2. The method of claim 1 wherein the binding agent is a monoclonal antibody.

3. The method of claim 2 wherein the binding agent is a polyclonal antibody.

4. A method for monitoring the progression of prostate cancer in a patient, comprising:

(a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;

(b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

10. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies of claim 5; and
- (b) a detection reagent.

11. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and
- (b) a detection reagent.

12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.

13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.

14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate

protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

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(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

(57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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INTERNATIONAL SEARCH REPORT

International Application No

PC., US 98/03690

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 6 G01N33/574 G01N33/577 G01N33/543 C07K16/30 C12Q1/68
 A61K39/395 A61K47/48

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category ¹	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 21671 A (UNIV COLUMBIA ;FISHER PAUL B (US); SHEN RUOQUIAN (US)) 18 July 1996 see the whole document ---	1-10, 12-22
A	EL-SHIRBINY A M: "PROSTATIC SPECIFIC ANTIGEN" ADVANCES IN CLINICAL CHEMISTRY, vol. 31, 1994, pages 99-133, XP000617158 see the whole document ---	1-10, 12-22
A	WO 93 14775 A (WRIGHT GEORGE L JR) 5 August 1993 see the whole document ---	1-10, 12-22 -/-

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

31 August 1998

Date of mailing of the international search report

30 DEC 1998

Name and mailing address of the ISA

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/JS 98/03690

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 94 09820 A (SLOAN KETTERING INST CANCER ;ISRAELI RON S (US); HESTON WARREN D W) 11 May 1994 see the whole document ---	1-10, 12-22
A	WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document ---	1-10, 12-22
A	ROBSON C N ET AL: "IDENTIFICATION OF PROSTATIC ANDROGEN REGULATED GENES USING THE DIFFERENTIAL DISPLAY TECHNIQUE" PROCEEDINGS OF THE ANNUAL MEETING OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH, TORONTO, MAR. 18 - 22, 1995, no. MEETING 86, 18 March 1995, AMERICAN ASSOCIATION FOR CANCER RESEARCH, page 266 XP002019344 see the whole document ---	1-10, 12-22
A	BLOK L J ET AL: "ISOLATION OF CDNAS THAT ARE DIFFERENTIALLY EXPRESSED BETWEEN ANDROGEN-DEPENDENT AND ANDROGEN-INDEPENDENT PROSTATE CARCINOMA CELLS USING DIFFERENTIAL DISPLAY PCR" PROSTATE, vol. 26, no. 4, April 1995, pages 213-224, XP000611577 see the whole document ---	1-10, 12-22
A	ALEXEYEV ET AL.: "IMPROVED ANTIBIOTIC-RESISTANCE GENE CASSETTES AND OMEGA ELEMENTS FOR E.COLI VECTOR CONSTRUCTION AND IN VITRO DELETION/INSERTION MUTAGENESIS" GENE, vol. 160, 1995, pages 63-67, XP002076033 & DATABASE EMBL AC: U35129, 1995 "pBSL141" see abstract ---	1-10, 12-22
P,A	DATABASE EMBL AC: AA453562, 11 June 1997 HILLIER ET AL.: "HOMO SAPIENS cDNA CLONE 788180" XP002075910 see abstract -----	1-10, 12-22

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/03690

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:

because they relate to subject matter not required to be searched by this Authority, namely:

Remark: Although claims 6 and 7 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2. Claims Nos.:

because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. Claims Nos.:

because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see FURTHER INFORMATION sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-10, 12-22 (all partially)

Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-10,12-22 (all partially)

Invention 1:

Methods and diagnostic kits for detecting and monitoring prostate cancer comprising either a binding agent capable of binding to a polypeptide encoded by a DNA molecule with Seq. ID 2 or oligonucleotide primers specific for a DNA molecule with Seq. ID 2 as well as an monoclonal antibody binding to a prostate protein encoded by a DNA molecule with Seq. ID 2 used in a method for inhibiting development of prostate cancer.

2. Claims: 1-10,12-22 (all partially)

Inventions 2-130:

Methods and diagnostic kits for detecting and monitoring prostate cancer comprising either a binding agent capable of binding to a polypeptide encoded by a DNA molecule with Seq. ID 3 or oligonucleotide primers specific for a DNA molecule with Seq. ID 3 as well as an monoclonal antibody binding to a prostate protein encoded by a DNA molecule with Seq. ID 3 used in a method for inhibiting development of prostate cancer.

...ibidem for Seq. ID 8-29,
41-45,47-52,54-65,70,73,74,79,81,87,90,92,93,97,103,104,107,1
15-160,171,181,188,191,193,194,198,203,204,207,209-211,220,22
2-224.

3. Claims: 1-4,8,9,11-22 (all partially)

Inventions 131-215:

Methods and diagnostic kits for detecting and monitoring prostate cancer comprising either a binding agent capable of binding to a polypeptide encoded by a DNA molecule with Seq. ID 5 or oligonucleotide primers specific for a DNA molecule with Seq. ID 5 as well as an monoclonal antibody binding to a prostate protein encoded by a DNA molecule with Seq. ID 5 used in a method for inhibiting development of prostate cancer.

...ibidem for each of Seq. ID
6,7,30-40,46,53,66-69,71,72,75-78,80,82-86,88,89,91,94-96,98-
102,105,106,161-170,179,180,182-187,189,190,192,195-197,198-2
02,205,206,208,212-219.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/03690

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 9621671 A	18-07-1996	AU 4751196 A CA 2209941 A EP 0804458 A		31-07-1996 18-07-1996 05-11-1997
WO 9314775 A	05-08-1993	CA 2106487 A		01-08-1993
WO 9409820 A	11-05-1994	CA 2147499 A EP 0668777 A JP 8506005 T US 5538866 A		11-05-1994 30-08-1995 02-07-1996 23-07-1996
WO 9504548 A	16-02-1995	AU 686660 B AU 7631294 A CA 2168952 A EP 0721345 A JP 9504000 T		12-02-1998 28-02-1995 16-02-1995 17-07-1996 22-04-1997